

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: April 21, 2006, 13:34:18 ; Search time 188 Seconds
(without alignments)
35.057 Million cell updates/sec

Title: US-09-993-399-1

Perfect score: 79

Sequence: 1 RHYETKXNQSRSSRS 15

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1000 summaries

Database :

A_Geneseq_21.*
1: Geneseqp1980s.*
2: Geneseqp1990s.*
3: Geneseqp2000s.*
4: Geneseqp2001s.*
5: Geneseqp2002s.*
6: Geneseqp2003as.*
7: Geneseqp2003bs.*
8: Geneseqp2004s.*
9: Geneseqp2005s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	79	100.0	15	6	ABR61469 Human dis
2	79	100.0	355	8	ADG89869 Human kin
3	79	100.0	355	9	ADV50412 Human kin
4	79	100.0	496	8	ADG89867 Human cen
5	79	100.0	2503	9	ADM44257 Human cen
6	79	100.0	2543	9	ADM44255 Human cen
7	79	100.0	2568	9	ADM44253 Human cen
8	79	100.0	2633	4	ABG06505 Novel hum
9	79	100.0	2663	4	AAM39097 Human pol
10	79	100.0	2663	8	ADQ17932 Human sof
11	79	100.0	2663	9	ADQ06867 Cyclin-de
12	79	100.0	2688	4	AAM40883 Human pol
13	69	87.3	2954	2	AAY01632 Amino aci
14	65	82.3	694	8	ADK97061 Plant ful
15	54	68.4	955	2	AAR57365 K39 polyp
16	54	68.4	955	2	AAR57365 K39 polyp
17	53	67.1	2013	4	ABE23222 Drosophil
18	52	65.8	154	3	AAB40661 Human ORF
19	52	65.8	154	5	ABP31636 Human str
20	52	65.8	341	5	ABG80079 Human kin
21	52	65.8	341	6	ABG72398 Human kin
22	52	65.8	348	6	ABR44339 Polypepti
23	52	65.8	1279	5	ABG80078 Human kin
24	52	65.8	1279	5	ABG70787 Human kin

25	52	65.8	1279	6	ABG72397	Abg72397 Human par
26	52	65.8	1401	7	ADJ94914	Adj94914 Novel NOV
27	52	65.8	1931	4	ABB61012	Abb61012 Drosophil
28	51	64.6	829	3	AAG31117	Aag31117 Arabidops
29	51	64.6	829	3	AAG31117	Aag31117 Arabidops
30	51	64.6	834	3	AAG31116	Aag31116 Arabidops
31	50	63.3	677	4	ABB65183	Abb65183 Drosophil
32	49	62.0	172	3	AGL14279	Ag14279 Arabidops
33	49	62.0	346	7	ADC23342	Adc23342 Human kin
34	49	62.0	346	8	ADQ60232	Adq60232 Human mic
35	49	62.0	346	8	ADQ88357	Adq88357 Human mic
36	49	62.0	370	7	ADC23338	Adc23338 Human kin
37	49	62.0	370	8	ADQ60228	Adq60228 Human mic
38	49	62.0	370	8	ADQ88353	Adq88353 Human mic
39	49	62.0	460	3	AAB56650	Aab56650 Human pro
40	49	62.0	487	7	ADC23344	Adc23344 Human kin
41	49	62.0	487	8	ADQ60234	Adq60234 Human mic
42	49	62.0	487	8	ADQ88359	Adq88359 Human mic
43	49	62.0	490	7	ADK40973	Adk40973 Novel hum
44	49	62.0	490	8	ADR15692	Adr15692 Kinase 73
45	49	62.0	512	7	ADC23340	Adc23340 Human kin
46	49	62.0	512	8	ADQ60230	Adq60230 Human mic
47	49	62.0	512	8	ADQ88355	Adq88355 Human mic
48	49	62.0	665	8	ADQ09240	Adq09240 Human KNS
49	49	62.0	665	8	ABM81748	Abm81748 Tumour-as
50	49	62.0	2033	9	ADZ13122	Adz13122 Murine ca
51	48	60.8	324	2	AAW70235	Aaw70235 Leishmani
52	48	60.8	324	5	AAE24949	Aae24949 Leishmani
53	48	60.8	324	5	AAU71831	Aau71831 Leishmani
54	48	60.8	324	5	ABG60887	Abg60887 Leishmani
55	48	60.8	324	5	ABG71285	Abg71285 L. chagas
56	48	60.8	324	7	ADB78816	Adb78816 Leishmani
57	47	59.5	54	5	ABB53101	Abb53101 Human ORF
58	47	59.5	458	8	ADX96421	Adx96421 Plant ful
59	47	59.5	670	8	ADN23314	Adn23314 Bacterial
60	47	59.5	754	8	ADN72187	Adn72187 Thale cre
61	46	58.2	398	3	AG21667	Ag21667 Arabidops
62	46	58.2	452	3	AG21666	Ag21666 Arabidops
63	46	58.2	469	3	AG21665	Ag21665 Arabidops
64	46	58.2	922	8	ADM67741	Adm67741 A. thalia
65	46	58.2	938	8	ADT04834	Adt04834 Thale cre
66	46	58.2	955	8	ADM67694	Adm67694 Tobacco N
67	46	58.2	955	8	ADT04787	Adt04787 Common to
68	45	57.0	191	4	ABB15077	Abb15077 Human ner
69	45	57.0	201	4	ADM19995	Adm19995 Protein e
70	45	57.0	315	5	ABB47850	Abb47850 Listeria
71	45	57.0	328	8	ADX76282	Adx76282 Plant ful
72	45	57.0	352	9	ADV50410	Adv50410 Human uKH
73	45	57.0	355	9	ADV50411	Adv50411 Human NKH
74	45	57.0	384	4	ADM19736	Adm19736 Protein e
75	45	57.0	411	2	AAW72745	Aaw72745 Drosophil
76	45	57.0	441	2	AAW72744	Aaw72744 Drosophil
77	45	57.0	441	2	AAW72744	Aaw72744 Drosophil
78	45	57.0	915	8	ADQ97735	Adq97735 Human can
79	45	57.0	956	7	ADB67086	Adb67086 Kinesin h
80	45	57.0	956	8	ADQ97732	Adq97732 Mouse can
81	45	57.0	956	9	ADB08337	Aeb08337 c-Jun inh
82	45	57.0	957	7	ADB67085	Adb67085 Kinesin h
83	45	57.0	959	8	ADL99356	Adl99356 Nanostruc
84	45	57.0	959	8	ADL99357	Adl99357 Nanostruc
85	45	57.0	963	4	AAM78880	Aam78880 Human pro
86	45	57.0	963	7	ADB67089	Adb67089 Kinesin h
87	45	57.0	963	7	ADB67091	Adb67091 Kinesin h
88	45	57.0	963	9	AEB08391	Aeb08391 c-Jun inh
89	45	57.0	964	8	ADL99362	Adl99362 Nanostruc
90	45	57.0	964	8	ADL99360	Adl99360 Nanostruc
91	45	57.0	967	7	ADB67090	Adb67090 Kinesin h
92	45	57.0	970	8	ADL99361	Adl99361 Nanostruc
93	45	57.0	975	2	AAW72746	Aaw72746 Drosophil
94	45	57.0	975	4	ABB63485	Abb63485 Drosophil
95	45	57.0	975	7	ADB67088	Adb67088 Kinesin h
96	45	57.0	975	8	ADL99359	Adl99359 Nanostruc
97	45	57.0	979	4	AAW79864	Aaw79864 Human pro

98	45	57.0	1011	6	ABR54195	AbR54195 Human NOV	171	40	50.6	205	5	AAE14609	Aae14609 Human mic
99	45	57.0	1011	7	ADK18370	AdK18370 Human NOV	172	40	50.6	205	6	ABU08213	Abu08213 Human kin
100	45	57.0	1027	7	ADB67096	AdB67096 Neuroal	173	40	50.6	205	6	ADA09079	Ada09079 Human gen
101	45	57.0	1027	8	ADL99367	AdL99367 Nanostruc	174	40	50.6	216	4	AAE03411	Aae03411 Human gen
102	45	57.0	1027	9	AEB08355	Aeb08355 c-Jun inh	175	40	50.6	302	4	AGS93108	AgS93108 C glutami
103	45	57.0	1031	7	ADB67093	AdB67093 Kinesin h	176	40	50.6	401	7	ADM05302	AdM05302 Human pro
104	45	57.0	1032	7	ADB67095	AdB67095 Neuroal	177	40	50.6	784	4	ABB71112	Abb71112 Drosophil
105	45	57.0	1032	8	ADL99366	AdL99366 Nanostruc	178	40	50.6	814	8	ADQ67765	AdQ67765 Novel hum
106	45	57.0	1032	8	ADL99364	AdL99364 Nanostruc	179	40	50.6	916	7	ADJ95102	AdJ95102 Novel NOV
107	45	57.0	1269	3	AAV77955	Aay77955 A. thalia	180	40	50.6	1003	4	ABB61405	Abb61405 Drosophil
108	45	57.0	1269	3	AAU92224	Aau92224 Thale cre	181	40	50.6	1142	4	AGS70713	AgS70713 S cerevis
109	44	55.7	348	4	ABU53208	Abu53208 Human cel	182	40	50.6	1142	6	ABR53123	AbR53123 Protein s
110	44	55.7	365	8	ADK73524	AdK73524 Plant ful	183	40	50.6	1142	7	ADR63074	AdR63074 Disease t
111	44	55.7	366	4	ABU53125	Abu53125 Intracell	184	40	50.6	1142	8	ADI26783	Adi26783 Saccharom
112	44	55.7	683	7	ABO77443	AbO77443 Pseudomon	185	40	50.6	1142	8	ADN19047	Adn19047 Bacterial
113	44	55.7	706	7	ADB67098	AdB67098 Kinesin-1	186	40	50.6	1226	8	ADQ36873	AdQ36873 Cell prol
114	44	55.7	706	8	ADL99369	AdL99369 Nanostruc	187	39	49.4	225	2	AAW60574	Aaw60574 Human tra
115	44	55.7	706	8	ADK44039	AdK44039 Bacterial	188	39	49.4	292	2	AAW60573	Aaw60573 Human tra
116	44	55.7	966	8	ADY06882	AdY06882 Plant ful	189	39	49.4	334	8	ADO22401	Ado22401 Candida a
117	43	54.4	337	5	ABB81634	Abb81634 Human kin	190	39	49.4	435	7	ABO76168	AbO76168 Pseudomon
118	43	54.4	337	6	ABO23390	AbO23390 Motor dom	191	39	49.4	451	6	ABU19416	Abu19416 Protein e
119	43	54.4	337	5	ABB86788	Abb86788 Motor dom	192	39	49.4	538	8	ADN99667	Adn99667 Novel hum
120	43	54.4	342	5	ABB81633	Abb81633 Human kin	193	39	49.4	792	7	ADRS5349	AdRS5349 Cyclin-de
121	43	54.4	342	6	AO233389	Aao233389 Human kin	194	39	49.4	796	7	ADO7217	Ado7217 Cyclin-de
122	43	54.4	342	7	ADB66786	AdB66786 Human mot	195	39	49.4	815	9	ADO22339	Ado22339 Candida a
123	43	54.4	365	9	ADV50409	Adv50409 Human KIF	196	39	49.4	884	7	ADM56288	AdM56288 Human ATP
124	43	54.4	672	7	ADY69858	AdY69858 Human bea	197	39	49.4	884	9	ADV85875	Adv85875 Zsea may
125	43	54.4	702	9	ADY17011	AdY17011 PRO polyp	198	39	49.4	887	8	ADT60761	Adt60761 Plant pol
126	43	54.4	954	8	ADM67697	AdM67697 Rice NACK	199	39	49.4	928	7	ADB67092	AdB67092 Kinesin h
127	43	54.4	954	8	ADT04805	AdT04805 Rice ster	200	39	49.4	928	7	ADL99363	AdL99363 Nanostruc
128	43	54.4	954	8	ADT04790	AdT04790 Japanese	201	39	49.4	932	8	ADN23372	Adn23372 Bacterial
129	43	54.4	955	8	ADY06857	AdY06857 Plant ful	202	39	49.4	1038	4	AAW67416	Aaw67416 Amino aci
130	43	54.4	955	8	ADM67692	AdM67692 Tobacco N	203	39	49.4	1038	6	ABG72691	AbG72691 Yeast cin
131	43	54.4	959	8	ADT04785	AdT04785 Common co	204	39	49.4	1038	7	ADG98858	AdG98858 Yeast cin
132	43	54.4	974	8	ADM67696	AdM67696 A. thalia	205	39	49.4	1038	8	ADN19055	Adn19055 Bacterial
133	43	54.4	974	8	ADT04789	AdT04789 Thale cre	206	38.5	48.7	297	4	ABG21264	AbG21264 Novel hum
134	43	54.4	1062	8	ADN25163	AdN25163 Fertility	207	38	48.1	297	4	ABR34053	AbR34053 Human can
135	43	54.4	1062	8	ADN61178	AdN61178 Radish nu	208	38	48.1	15	6	ABR34001	AbR34001 Human can
136	43	54.4	1062	8	ADJ95086	AdJ95086 Novel NOV	209	38	48.1	15	6	ABR33807	AbR33807 Human can
137	43	54.4	1324	7	ADU73907	AdU73907 Human str	210	38	48.1	15	6	ABR33913	AbR33913 Human can
138	43	54.4	1342	8	ADX74336	AdX74336 Plant ful	211	38	48.1	15	6	ABR34047	AbR34047 Human can
139	42	53.2	213	8	ADY74336	AdY74336 Human HK	212	38	48.1	15	6	ABR34046	AbR34046 Human can
140	42	53.2	326	5	ABU08248	Abu08248 Human HK	213	38	48.1	15	6	ABR33945	AbR33945 Human can
141	42	53.2	326	5	AAU99336	Aau99336 Truncated	214	38	48.1	15	6	AAU66998	Aau66998 Propionib
142	42	53.2	326	7	ADF67464	Adf67464 Human HK	215	38	48.1	59	4	AAU55225	Aau55225 Propionib
143	42	53.2	326	7	ADN07557	Adn07557 Human kin	216	38	48.1	59	4	ABM63517	Abm63517 Propionib
144	42	53.2	326	8	ADN07557	Adn07557 Bacterial	217	38	48.1	59	6	ABM51744	Abm51744 Propionib
145	42	53.2	517	8	ADS23848	Ads23848 Human str	218	38	48.1	166	4	AAU16200	Aau16200 Human nov
146	42	53.2	626	6	ABP98830	Abp98830 Plant ful	219	38	48.1	166	6	ABU55269	Abu55269 Human nov
147	42	53.2	676	8	ADX74357	AdX74357 Human HK	220	38	48.1	183	5	ABP27778	Abp27778 Streptoco
148	42	53.2	787	5	ABU09335	Aau09335 Human kin	221	38	48.1	190	2	AAW60576	Aaw60576 Human tra
149	42	53.2	787	7	ADF67462	Adf67462 Human HK	222	38	48.1	190	6	ABR57489	AbR57489 Human tra
150	42	53.2	787	8	ADN07555	Adn07555 Human kin	223	38	48.1	190	6	ABR01799	AbR01799 Human can
151	42	53.2	792	7	ADN07555	Adn07555 Human kin	224	38	48.1	190	6	ABR01844	AbR01844 Human can
152	42	53.2	1218	4	ADCL0188	Adcl0188 Human NOV	225	38	48.1	190	6	ADQ17562	AdQ17562 Human sof
153	41	51.9	175	6	ABU61495	Abu61495 Drosophil	226	38	48.1	202	2	AAW60575	Aaw60575 Human tra
154	41	51.9	317	8	ADX74071	AdX74071 Plant ful	227	38	48.1	215	4	ABU50237	Abu50237 Human tra
155	41	51.9	397	8	ADY09598	AdY09598 Plant ful	228	38	48.1	215	6	ABU19608	Abu19608 Protein e
156	41	51.9	534	7	ADN09598	Adn09598 Rice abio	229	38	48.1	323	6	ADY09251	AdY09251 Plant ful
157	41	51.9	573	8	ADN09598	Adn09598 Bacterial	230	38	48.1	324	6	ABU26361	Abu26361 Protein e
158	41	51.9	614	8	ADQ36847	Adq36847 Cell prol	231	38	48.1	331	6	ABR57488	AbR57488 Human SHO
159	41	51.9	658	8	ADX91654	Adx91654 Plant ful	232	38	48.1	331	6	ABR01845	AbR01845 Human can
160	41	51.9	690	8	ADS23762	Ads23762 Bacterial	233	38	48.1	335	8	ADX72542	AdX72542 Plant ful
161	41	51.9	788	8	ADN21210	Adn21210 Bacterial	234	38	48.1	335	5	AAE14401	Aae14401 Human HK
162	40	50.6	123	3	AGL14103	AgL14103 Arabidops	235	38	48.1	375	5	AAU79591	Aau79591 Human HK
163	40	50.6	150	3	AGL14102	AgL14102 Arabidops	236	38	48.1	409	5	AAE14402	Aae14402 Human HK
164	40	50.6	160	3	AAE03385	Aae03385 Human gen	237	38	48.1	409	5	AAU79592	Aau79592 Human HK
165	40	50.6	160	5	ABG63679	Abg63679 Human alb	238	38	48.1	463	8	ABR70668	AbR70668 Drosophil
166	40	50.6	160	5	ADL76944	Adl76944 Albumin f	239	38	48.1	505	8	ADY89129	AdY89129 Plant ful
167	40	50.6	168	3	AGL14101	AgL14101 Arabidops	240	38	48.1	515	8	ADY22863	AdY22863 Plant ful
168	40	50.6	168	3	AGL14101	AgL14101 Arabidops	241	38	48.1	562	8	ADX72393	AdX72393 Plant ful
169	40	50.6	184	3	AGS31633	AgS31633 Arabidops	242	38	48.1	590	7	ABO80243	AbO80243 Pseudomon
170	40	50.6	202	3	AGS31632	AgS31632 Arabidops	243	38	48.1				

244	38	48.1	5	ABP43566	Abp43566 Human ehe	317	37	45.8	890	8	ADQ15056	Adq15056 Human can	
245	38	48.1	602	4	ABP90821	Abp90821 Human she	318	37	890	8	ADU46859	Adu46859 RAB6 ince	
246	38	48.1	663	4	AAE502777	AAe502777 Human PRO	319	37	890	9	ADY17476	Ady17476 PRO polyyp	
247	38	48.1	663	5	AAU97912	AAu97912 Human PRO	320	37	46.8	925	3	AAO13881	Aao13881 Human pol
248	38	48.1	663	7	ADC51455	Adc51455 Human mac	321	37	46.8	957	3	AAQ30696	Aaq30696 Arabidops
249	38	48.1	663	7	ADG25731	Adg25731 Human pro	322	37	46.8	960	3	AAQ30695	Aaq30695 Arabidops
250	38	48.1	680	4	ABG63472	Abg63472 Drosophil	323	37	46.8	960	5	ABG92950	Abg92950 Herbicida
251	38	48.1	718	6	ABU49055	Abu49055 Protein e	324	37	46.8	960	5	ABG30877	Abg30877 A. thalia
252	38	48.1	729	9	ADV77108	Adv77108 Huntingto	325	37	46.8	960	6	ADA01390	Ada01390 A. thalia
253	38	48.1	753	9	AEb40556	Aeb40556 L. pneumo	326	37	46.8	993	8	ADQ19013	Adq19013 Human sof
254	38	48.1	774	9	AEb37220	Aeb37220 L. pneumo	327	37	46.8	1016	8	ADR20367	Adr20367 Reconbina
255	38	48.1	873	8	ADQ76433	Adq76433 Amino aci	328	37	46.8	1016	8	ADR21496	Adr21496 Xenorhabd
256	38	48.1	888	4	AAE06695	AAe06695 Arabidops	329	37	46.8	1029	5	AAE17786	Aae17786 Human kin
257	38	48.1	888	8	ADN72911	Adn72911 Thale cre	330	37	46.8	1029	5	ADC10190	Adc10190 Human NOV
258	38	48.1	888	8	ADN73171	Adn73171 Thale cre	331	37	46.8	1034	3	AAQ31112	Aaq31112 Arabidops
259	38	48.1	992	8	ADT57826	Adt57826 Plant pol	332	37	46.8	1069	3	AAQ31111	Aaq31111 Arabidops
260	38	48.1	1030	8	ADY06933	Ady06933 Plant ful	333	37	46.8	1087	6	ABP57673	Abp57673 HIF-1 alp
261	38	48.1	1388	5	AAE14400	AAe14400 Human kin	334	37	46.8	1121	3	AAQ31110	Aaq31110 Arabidops
262	38	48.1	1388	5	AAU79590	AAu79590 Human kin	335	37	46.8	1122	6	ABP57675	Abp57675 HIF-1 alp
263	38	48.1	1388	6	ABR48222	ABr48222 Human bla	336	37	46.8	1125	6	ABP57672	Abp57672 HIF-1 alp
264	38	48.1	1388	7	ABR80468	ABr80468 Ovarian c	337	37	46.8	1160	6	ABP57674	Abp57674 HIF-1 alp
265	38	48.1	1388	7	ADC35116	Adc35116 Human bre	338	37	46.8	1269	2	AAW03659	AAw03659 RPP5 down
266	38	48.1	1388	8	ADL83290	Adl83290 Human PRO	339	37	46.8	1274	4	ABE65781	ABe65781 Drosophil
267	38	48.1	1388	8	ADQ20128	Adq20128 Human sof	340	37	46.8	1274	9	ABE16334	ABe16334 Fruit fly
268	38	48.1	1388	8	ADQ09226	Adq09226 Human RNS	341	37	46.8	1474	7	AAE39593	AAe39593 Drosophil
269	38	48.1	1388	9	AEA62054	AEa62054 Human kin	342	37	46.8	1500	4	ABE63715	ABe63715 Drosophil
270	37	46.8	64	4	AAU43043	AAu43043 Propionib	343	37	46.8	1503	7	AAE39594	AAe39594 Drosophil
271	37	46.8	64	6	ABM39562	ABm39562 Propionib	344	37	46.8	1509	7	AAE39592	AAe39592 Drosophil
272	37	46.8	87	4	ABG65040	ABg65040 Drosophil	345	37	46.8	1318	4	ABE61958	ABe61958 Drosophil
273	37	46.8	87	8	ADQ07971	Adq07971 Fly polyyp	346	36	46.2	247	4	ABG23162	ABg23162 Novel hum
274	37	46.8	120	4	ADQ078737	Adq078737 Phosphona	347	36	45.6	61	3	AAQ00127	AAq00127 Human sec
275	37	46.8	137	2	AAW64594	AAw64594 Rabbit J	348	36	45.6	72	4	ABE41362	ABe41362 Peptide #
276	37	46.8	137	2	AAW61573	AAw61573 Rabbit J	349	36	45.6	72	4	AAW35150	AAw35150 Peptide #
277	37	46.8	137	2	AAW85747	AAw85747 J chain s	350	36	45.6	72	4	ABE25299	ABe25299 Protein #
278	37	46.8	137	5	ABG94816	ABg94816 Rabbit J	351	36	45.6	72	4	AAW75034	AAw75034 Human bon
279	37	46.8	137	5	ABG68245	ABg68245 Rabbit J	352	36	45.6	72	4	AAU59486	AAu59486 Propionib
280	37	46.8	137	8	ADH61859	ADh61859 Mouse J c	353	36	45.6	72	4	AAW62230	AAw62230 Human bra
281	37	46.8	159	2	AAW71890	AAw71890 Anti-huma	354	36	45.6	72	4	ABG56803	ABg56803 Human liv
282	37	46.8	159	3	AAE12910	AAe12910 Anti-huma	355	36	45.6	72	6	ABM56005	ABm56005 Propionib
283	37	46.8	209	4	ABG03132	ABg03132 Novel hum	356	36	45.6	79	5	ABP38302	ABp38302 Staphyloc
284	37	46.8	290	7	ADM25686	Adm25686 Hyperther	357	36	45.6	79	8	ADG04766	Adg04766 Staphyloc
285	37	46.8	329	5	AAE17787	AAe17787 Human kin	358	36	45.6	88	4	AAU48647	AAu48647 Propionib
286	37	46.8	382	8	ADQ05898	Adq05898 C. albica	359	36	45.6	88	6	ABM45166	ABm45166 Propionib
287	37	46.8	382	8	ADQ05894	Adq05894 C. albica	360	36	45.6	99	4	AAU54137	AAu54137 Propionib
288	37	46.8	401	8	ADN21136	ADn21136 Bacterial	361	36	45.6	99	6	ABM50656	ABm50656 Propionib
289	37	46.8	431	4	AAE85506	AAe85506 Human pro	362	36	45.6	182	8	ADS44591	ADs44591 Bacterial
290	37	46.8	445	6	ABU21623	ABu21623 Protein e	363	36	45.6	204	5	ABO67490	ABo67490 Klebsiell
291	37	46.8	457	9	ABM92762	ABm92762 M. xanthu	364	36	45.6	204	5	ABB48449	ABb48449 Listeria
292	37	46.8	490	4	ABG23354	ABg23354 Novel hum	365	36	45.6	248	2	AAW72906	AAw72906 Mycobacte
293	37	46.8	500	3	AAQ21939	AAq21939 Arabidops	366	36	45.6	248	2	AAQ21923	AAq21923 Amino aci
294	37	46.8	528	6	ABU56420	ABu56420 Lung canc	367	36	45.6	299	6	ABU22539	ABu22539 Protein e
295	37	46.8	528	7	ADB80539	ADB80539 Ovarian c	368	36	45.6	317	6	ABP57736	ABp57736 S. pombe
296	37	46.8	538	8	ADQ05892	Adq05892 C. albica	369	36	45.6	321	4	ABE52869	ABe52869 Escherich
297	37	46.8	538	8	ADQ05896	Adq05896 C. albica	370	36	45.6	340	9	ADM46619	ADm46619 Salmonid
298	37	46.8	538	8	ABO59509	ABo59509 Human gen	371	36	45.6	361	5	ABE08099	ABe08099 Human HSE
299	37	46.8	575	3	AAQ21938	AAq21938 Arabidops	372	36	45.6	361	5	ABU63118	ABu63118 Human kin
300	37	46.8	575	3	ABO64082	ABo64082 Klebsiell	373	36	45.6	361	8	ADS13628	ADs13628 Human HSE
301	37	46.8	598	3	AAQ21937	AAq21937 Arabidops	374	36	45.6	369	5	ABB08101	ABb08101 Human HSE
302	37	46.8	600	9	ADY49879	Ady49879 Fumarate	375	36	45.6	369	6	ABU63120	ABu63120 Human kin
303	37	46.8	602	8	ADG45237	ADg45237 Bacterial	376	36	45.6	369	8	ADS13632	ADs13632 Human HSE
304	37	46.8	602	9	ADY80487	ADy80487 Non-amino	377	36	45.6	370	5	ABE08100	ABe08100 Human HSE
305	37	46.8	627	2	AAW85710	AAw85710 Grand fir	378	36	45.6	370	6	ABU63119	ABu63119 Human kin
306	37	46.8	627	4	AAE69380	AAe69380 Grand fir	379	36	45.6	370	8	ADS13630	ADs13630 Human HSE
307	37	46.8	627	5	ABR79395	ABr79395 Taxadiene	380	36	45.6	374	8	ADQ67675	ADq67675 Novel hum
308	37	46.8	729	4	ABE59500	ABe59500 Drosophil	381	36	45.6	375	9	AEAl7501	AEa17501 Braggica
309	37	46.8	811	6	ABR58290	ABr58290 BCU0343 p	382	36	45.6	384	2	AAE34649	AAe34649 Heparinas
310	37	46.8	811	6	ABR58329	ABr58329 XM_035861	383	36	45.6	384	2	AAW28545	AAw28545 Mutant po
311	37	46.8	865	6	ABR41371	ABr41371 Human DIT	384	36	45.6	384	3	AAQ70186	AAq70186 Mutant F.
312	37	46.8	868	6	ABR41418	ABr41418 Human DIT	385	36	45.6	384	3	AAQ70195	AAq70195 Mutant F.
313	37	46.8	870	5	ABP69487	ABp69487 Human pol	386	36	45.6	384	3	AAQ70174	AAq70174 Modified
314	37	46.8	884	6	ABU05307	ABu05307 Human dia	387	36	45.6	384	3	AAQ70190	AAq70190 Mutant F.
315	37	46.8	890	6	ABR922143	ABr922143 Human cer	388	36	45.6	384	3	AAQ70180	AAq70180 Mutant F.
316	37	46.8	890	8	ADQ09274	Adq09274 Human RAB	389	36	45.6	384	3	AAQ70184	AAq70184 Mutant F.

390	36	45.6	384	3	AAy70187	AAy70187 Mutant F.	463	36	45.6	1815	8	ADR66952	Adr66952 Human pro
391	36	45.6	384	3	AAy70159	AAy70159 F. hepari	464	36	45.6	1815	8	ADR66054	Adr66054 Human pro
392	36	45.6	384	3	AAy70189	AAy70189 Mutant F.	465	36	45.6	1815	8	ADR66951	Adr66951 Human pro
393	36	45.6	384	3	AAy70192	AAy70192 Mutant F.	466	36	45.6	1815	8	ADR66053	Adr66053 Human pro
394	36	45.6	384	3	AAy70175	AAy70175 Mutant F.	467	36	45.6	1826	7	ADU69671	Adj69671 Human hea
395	36	45.6	384	3	AAy70193	AAy70193 Mutant F.	468	36	45.6	1826	7	ADL83235	Adl83235 Human PRO
396	36	45.6	384	3	AAy70176	AAy70176 Mutant F.	469	36	45.6	1844	8	ADQ97522	Adq97522 Mouse can
397	36	45.6	384	3	AAy70188	AAy70188 Mutant F.	470	36	45.6	2732	7	ABM86028	Abm86028 Rice abio
398	36	45.6	384	3	AAy70188	AAy70188 Mutant F.	471	35.5	44.9	456	4	ABB66306	Abb66306 Drosophil
399	36	45.6	384	3	AAy70178	AAy70178 Mutant F.	472	35	44.3	11	2	AAE51685	AAr51685 Basophil
400	36	45.6	384	3	AAy70177	AAy70177 Mutant F.	473	35	44.3	117	4	ABG20543	Abg20543 Novel hum
401	36	45.6	384	3	AAy70194	AAy70194 Mutant F.	474	35	44.3	122	4	ABBS3081	Abbs3081 Escherich
402	36	45.6	384	3	AAy70179	AAy70179 Mutant F.	475	35	44.3	123	4	AAO05831	Aao05831 Human pol
403	36	45.6	384	3	AAy70182	AAy70182 Mutant F.	476	35	44.3	126	6	ABM72416	Abm72416 Staphyloc
404	36	45.6	384	3	AAy70181	AAy70181 Mutant F.	477	35	44.3	130	4	AAU30136	Aau30136 Novel hum
405	36	45.6	384	3	AAy70191	AAy70191 Mutant F.	478	35	44.3	137	3	ABZ52530	Abz52530 Pinus rad
406	36	45.6	384	3	AAy70185	AAy70185 Mutant F.	479	35	44.3	138	4	AAU46015	Aau46015 Propionib
407	36	45.6	384	4	ABB06931	Abb06931 Flavobact	480	35	44.3	138	6	ABM42534	Abm42534 Human EST
408	36	45.6	384	4	ADT92303	Adt92303 Pedobacte	481	35	44.3	158	4	ABBS59731	Abbs59731 Drosophil
409	36	45.6	401	5	ABU05531	Abu05531 M. tuberc	482	35	44.3	162	4	ABBS2688	Abbs2688 Escherich
410	36	45.6	415	4	ABU53207	Abu53207 Human cel	483	35	44.3	165	5	ABBS4613	Abbs4613 Lactococc
411	36	45.6	421	4	ABW70452	Abw70452 Drosophil	484	35	44.3	165	8	ADY12092	Ady12092 Plant ful
412	36	45.6	423	7	ABM87393	Abm87393 Rice abio	485	35	44.3	168	5	ABBS4467	Abbs4467 Lactococc
413	36	45.6	433	8	ADX78598	Adx78598 Plant ful	486	35	44.3	168	5	ABBS29372	Abbs29372 Bacterial
414	36	45.6	445	6	ADU22208	Adu22208 Protein e	487	35	44.3	194	2	AAI10915	Aai10915 Amino aci
415	36	45.6	475	8	ADX88307	Adx88307 Plant ful	488	35	44.3	194	2	ADY48058	Ady48058 Novel hum
416	36	45.6	503	3	ABE63190	AbE63190 Human sec	489	35	44.3	194	8	ADJ55613	Adj55613 Novel hum
417	36	45.6	519	9	ADX06347	Adx06347 Cyclin-de	490	35	44.3	194	8	AY57764	Ay57764 Rat l-sel
418	36	45.6	531	4	ABU53203	Abu53203 Human cel	491	35	44.3	196	3	AAV57764	Aav57764 Acinetoba
419	36	45.6	581	9	ADZ04438	Adz04438 Rice DIM1	492	35	44.3	233	3	AAI12947	Aai12947 Arabidops
420	36	45.6	583	6	ABU49710	Abu49710 Protein e	493	35	44.3	233	3	AG45830	Ag45830 Arabidops
421	36	45.6	626	4	ABBS59733	Abbs59733 Drosophil	494	35	44.3	237	4	ABG01227	Abg01227 Novel hum
422	36	45.6	626	4	ABU53205	Abu53205 Human cel	495	35	44.3	238	4	ABG23838	Abg23838 Novel hum
423	36	45.6	666	8	ADX911744	Adx911744 Plant ful	496	35	44.3	238	4	AAU30135	Aau30135 Novel hum
424	36	45.6	667	8	ADY13219	Ady13219 Plant ful	497	35	44.3	269	6	ABR41661	Abr41661 Human DIT
425	36	45.6	673	4	AAW38739	Aam38739 Human pol	498	35	44.3	275	6	ADA36537	Ada36527 Acinetoba
426	36	45.6	674	4	ABU53204	Abu53204 Human cel	499	35	44.3	281	8	ADT92014	Adt92014 Rabbit DN
427	36	45.6	684	4	ABU53206	Abu53206 Human cel	500	35	44.3	294	8	ADT58833	Adt58833 Plant pol
428	36	45.6	696	7	ADY69261	Ady69261 Human hea	501	35	44.3	296	6	ABBS9662	Abbs9662 Amino aci
429	36	45.6	749	8	ADY23039	Ady23039 Human hea	502	35	44.3	304	4	AAU30140	Aau30140 Novel hum
430	36	45.6	753	3	AAW08316	Aaw08316 A human M	503	35	44.3	306	4	ABE5020	AbE5020 Human sec
431	36	45.6	757	4	AAU19569	Aau19569 Human dia	504	35	44.3	308	8	ADY04206	Ady04206 Plant ful
432	36	45.6	757	5	ABP51294	Abp51294 Human MDD	505	35	44.3	317	6	ABU36081	Abu36081 Protein e
433	36	45.6	757	5	ABP51294	Abp51294 Human MDD	506	35	44.3	323	8	ADY171324	Ady171324 Plant ful
434	36	45.6	757	5	ABP51294	Abp51294 Human MDD	507	35	44.3	325	7	ADY171324	Ady171324 Plant ful
435	36	45.6	762	5	ABG60124	Abg60124 Human DIT	508	35	44.3	326	3	AAI12946	Aai12946 Mycobacte
436	36	45.6	776	4	AAW40525	Aaw40525 Human pol	509	35	44.3	326	3	AAI12946	Aai12946 Mycobacte
437	36	45.6	782	4	ABBS11348	Abbs11348 Human kin	510	35	44.3	326	6	ABU00080	Abu00080 Human nov
438	36	45.6	803	7	ADK11354	Adk11354 Drosophil	511	35	44.3	326	8	ADN73829	Adn73829 Thale cre
439	36	45.6	803	7	ADK11354	Adk11354 Drosophil	512	35	44.3	326	8	ADN73829	Adn73829 Thale cre
440	36	45.6	803	7	ADK11354	Adk11354 Drosophil	513	35	44.3	333	3	AAI12945	Aai12945 Arabidops
441	36	45.6	803	7	ADK11354	Adk11354 Drosophil	514	35	44.3	333	3	AAI12945	Aai12945 Arabidops
442	36	45.6	803	7	ADK11354	Adk11354 Drosophil	515	35	44.3	333	3	AAI12945	Aai12945 Arabidops
443	36	45.6	803	7	ADK11354	Adk11354 Drosophil	516	35	44.3	333	3	AAI12945	Aai12945 Arabidops
444	36	45.6	803	7	ADK11354	Adk11354 Drosophil	517	35	44.3	333	3	AAI12945	Aai12945 Arabidops
445	36	45.6	803	7	ADK11354	Adk11354 Drosophil	518	35	44.3	333	3	AAI12945	Aai12945 Arabidops
446	36	45.6	803	7	ADK11354	Adk11354 Drosophil	519	35	44.3	333	3	AAI12945	Aai12945 Arabidops
447	36	45.6	803	7	ADK11354	Adk11354 Drosophil	520	35	44.3	333	3	AAI12945	Aai12945 Arabidops
448	36	45.6	803	7	ADK11354	Adk11354 Drosophil	521	35	44.3	333	3	AAI12945	Aai12945 Arabidops
449	36	45.6	803	7	ADK11354	Adk11354 Drosophil	522	35	44.3	333	3	AAI12945	Aai12945 Arabidops
450	36	45.6	803	7	ADK11354	Adk11354 Drosophil	523	35	44.3	333	3	AAI12945	Aai12945 Arabidops
451	36	45.6	803	7	ADK11354	Adk11354 Drosophil	524	35	44.3	333	3	AAI12945	Aai12945 Arabidops
452	36	45.6	803	7	ADK11354	Adk11354 Drosophil	525	35	44.3	333	3	AAI12945	Aai12945 Arabidops
453	36	45.6	803	7	ADK11354	Adk11354 Drosophil	526	35	44.3	333	3	AAI12945	Aai12945 Arabidops
454	36	45.6	803	7	ADK11354	Adk11354 Drosophil	527	35	44.3	333	3	AAI12945	Aai12945 Arabidops
455	36	45.6	803	7	ADK11354	Adk11354 Drosophil	528	35	44.3	333	3	AAI12945	Aai12945 Arabidops
456	36	45.6	803	7	ADK11354	Adk11354 Drosophil	529	35	44.3	333	3	AAI12945	Aai12945 Arabidops
457	36	45.6	803	7	ADK11354	Adk11354 Drosophil	530	35	44.3	333	3	AAI12945	Aai12945 Arabidops
458	36	45.6	803	7	ADK11354	Adk11354 Drosophil	531	35	44.3	333	3	AAI12945	Aai12945 Arabidops
459	36	45.6	803	7	ADK11354	Adk11354 Drosophil	532	35	44.3	333	3	AAI12945	Aai12945 Arabidops
460	36	45.6	803	7	ADK11354	Adk11354 Drosophil	533	35	44.3	333	3	AAI12945	Aai12945 Arabidops
461	36	45.6	803	7	ADK11354	Adk11354 Drosophil	534	35	44.3	333	3	AAI12945	Aai12945 Arabidops
462	36	45.6	803	7	ADK11354	Adk11354 Drosophil	535	35	44.3	333	3	AAI12945	Aai12945 Arabidops

536	35	44.3	340	9	ADW46644	Adw46644	Salmonid	609	35	44.3	348	3	AAG27818	Arabidops
537	35	44.3	340	9	ADW46650	Adw46650	Salmonid	610	35	44.3	350	8	ADN04058	Antipsori
538	35	44.3	340	9	ADW46652	Adw46652	Salmonid	611	35	44.3	350	8	ADX06150	Cyclin-de
539	35	44.3	340	9	ADW46606	Adw46606	Salmonid	612	35	44.3	362	6	ABU00077	Human nov
540	35	44.3	340	9	ADW46612	Adw46612	Salmonid	613	35	44.3	365	9	ADV50414	Human KIF
541	35	44.3	340	9	ADW46625	Adw46625	Salmonid	614	35	44.3	369	7	ADU08029	Novel pro
542	35	44.3	340	9	ADW46627	Adw46627	Salmonid	615	35	44.3	369	9	ADU40399	Novel hum
543	35	44.3	340	9	ADW46639	Adw46639	Salmonid	616	35	44.3	370	4	ABG23842	Novel hum
544	35	44.3	340	9	ADW46589	Adw46589	Salmonid	617	35	44.3	372	7	ABE61903	Rat Prote
545	35	44.3	340	9	ADW46591	Adw46591	Salmonid	618	35	44.3	381	6	ABU00078	Human nov
546	35	44.3	340	9	ADW46614	Adw46614	Salmonid	619	35	44.3	394	5	AAO17206	Human sec
547	35	44.3	340	9	ADW46643	Adw46643	Salmonid	620	35	44.3	394	5	ABG64749	Human alb
548	35	44.3	340	9	ADW46658	Adw46658	Salmonid	621	35	44.3	394	8	ADL78016	Albumin f
549	35	44.3	340	9	ADW46662	Adw46662	Salmonid	622	35	44.3	395	7	ADM05932	Human pro
550	35	44.3	340	9	ADW46594	Adw46594	Salmonid	623	35	44.3	399	3	AAG27817	Arabidops
551	35	44.3	340	9	ADW46598	Adw46598	Salmonid	624	35	44.3	404	6	ADA35193	Acinetoba
552	35	44.3	340	9	ADW46629	Adw46629	Salmonid	625	35	44.3	407	9	ADU40584	Novel hum
553	35	44.3	340	9	ADW46636	Adw46636	Salmonid	626	35	44.3	408	7	ADC21265	Plasmodi
554	35	44.3	340	9	ADW46588	Adw46588	Salmonid	627	35	44.3	412	5	ABP53641	Medicago
555	35	44.3	340	9	ADW46605	Adw46605	Salmonid	628	35	44.3	414	8	ADX71432	Plant ful
556	35	44.3	340	9	ADW46609	Adw46609	Salmonid	629	35	44.3	419	4	ABG44997	Human sec
557	35	44.3	340	9	ADW46646	Adw46646	Salmonid	630	35	44.3	421	4	AAW41820	Human pol
558	35	44.3	340	9	ADW46603	Adw46603	Salmonid	631	35	44.3	422	8	ADT57719	Plant pol
559	35	44.3	340	9	ADW46653	Adw46653	Salmonid	632	35	44.3	435	7	ABO63465	Klebsiell
560	35	44.3	340	9	ADW46585	Adw46585	Salmonid	633	35	44.3	439	7	ADM05041	Human pro
561	35	44.3	340	9	ADW46607	Adw46607	Salmonid	634	35	44.3	443	4	AAU30139	Novel hum
562	35	44.3	340	9	ADW46615	Adw46615	Salmonid	635	35	44.3	444	8	ADX92254	Plant ful
563	35	44.3	340	9	ADW46617	Adw46617	Salmonid	636	35	44.3	450	4	AAAG64208	Murine pr
564	35	44.3	340	9	ADW46623	Adw46623	Salmonid	637	35	44.3	450	8	ADX92628	Plant ful
565	35	44.3	340	9	ADW46631	Adw46631	Salmonid	638	35	44.3	454	4	AAU54429	Propionib
566	35	44.3	340	9	ADW46654	Adw46654	Salmonid	639	35	44.3	454	6	ABM50948	ABM50948
567	35	44.3	340	9	ADW46559	Adw46559	Salmonid	640	35	44.3	468	5	ABG97352	Human CGD
568	35	44.3	340	9	ADW46663	Adw46663	Salmonid	641	35	44.3	473	5	ABG70992	Human car
569	35	44.3	340	9	ADW46586	Adw46586	Salmonid	642	35	44.3	474	7	ABM86533	Rice abio
570	35	44.3	340	9	ADW46596	Adw46596	Salmonid	643	35	44.3	479	9	ABE38253	L. pneumo
571	35	44.3	340	9	ADW46602	Adw46602	Salmonid	644	35	44.3	481	8	ADX73714	Plant ful
572	35	44.3	340	9	ADW46635	Adw46635	Salmonid	645	35	44.3	495	4	ABN94224	Human pro
573	35	44.3	340	9	ADW46637	Adw46637	Salmonid	646	35	44.3	506	5	AAE21173	Human TRI
574	35	44.3	340	9	ADW46641	Adw46641	Salmonid	647	35	44.3	522	5	ABG70991	Human HbK
575	35	44.3	340	9	ADW46647	Adw46647	Salmonid	648	35	44.3	542	8	ADY12421	Plant ful
576	35	44.3	340	9	ADW46655	Adw46655	Salmonid	649	35	44.3	549	8	ADY08818	Plant ful
577	35	44.3	340	9	ADW46590	Adw46590	Salmonid	650	35	44.3	550	4	ABG16717	Novel hum
578	35	44.3	340	9	ADW46593	Adw46593	Salmonid	651	35	44.3	554	7	ADJ71145	Human hema
579	35	44.3	340	9	ADW46608	Adw46608	Salmonid	652	35	44.3	562	8	ADS21149	Bacterial
580	35	44.3	340	9	ADW46642	Adw46642	Salmonid	653	35	44.3	563	8	ADN18322	Bacterial
581	35	44.3	340	9	ADW46645	Adw46645	Salmonid	654	35	44.3	571	8	ADN17386	Bacterial
582	35	44.3	340	9	ADW46664	Adw46664	Salmonid	655	35	44.3	628	4	ABE62327	Drosophil
583	35	44.3	340	9	ADW46561	Adw46561	Salmonid	656	35	44.3	631	6	ADB07316	Alloiooc
584	35	44.3	340	9	ADW46597	Adw46597	Salmonid	657	35	44.3	632	3	AAV66689	Membrane-
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586	35	44.3	340	9	ADW46632	Adw46632	Salmonid	659	35	44.3	632	4	AAAG78630	Plasmolem
587	35	44.3	340	9	ADW46634	Adw46634	Salmonid	660	35	44.3	632	4	AAU29106	Human PRO
588	35	44.3	340	9	ADW46601	Adw46601	Salmonid	661	35	44.3	632	4	AAAM39084	Human pol
589	35	44.3	340	9	ADW46628	Adw46628	Salmonid	662	35	44.3	632	4	AAAB87545	Human PRO
590	35	44.3	340	9	ADW46665	Adw46665	Salmonid	663	35	44.3	632	4	AAAB65212	Human PRO
591	35	44.3	340	9	ADW46595	Adw46595	Salmonid	664	35	44.3	632	5	ABG958670	Human sec
592	35	44.3	340	9	ADW46600	Adw46600	Salmonid	665	35	44.3	632	6	ABU58482	Human PRO
593	35	44.3	340	9	ADW46610	Adw46610	Salmonid	666	35	44.3	632	6	ABU88030	Novel hum
594	35	44.3	340	9	ADW46611	Adw46611	Salmonid	667	35	44.3	632	6	ABU84345	Human aec
595	35	44.3	340	9	ADW46616	Adw46616	Salmonid	668	35	44.3	632	6	ABR66219	Human aec
596	35	44.3	340	9	ADW46621	Adw46621	Salmonid	669	35	44.3	632	6	ABR65609	Human sec
597	35	44.3	340	9	ADW46640	Adw46640	Salmonid	670	35	44.3	632	6	ABU99549	Human sec
598	35	44.3	340	9	ADW46660	Adw46660	Salmonid	671	35	44.3	632	6	ABU58027	Human PRO
599	35	44.3	340	9	ADW46667	Adw46667	Salmonid	672	35	44.3	632	6	ABU59105	Novel hum
600	35	44.3	340	9	ADW46587	Adw46587	Salmonid	673	35	44.3	632	6	ABU82617	Human aec
601	35	44.3	340	9	ADW46630	Adw46630	Salmonid	674	35	44.3	632	6	ABU82788	Human PRO
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603	35	44.3	340	9	ADW46657	Adw46657	Salmonid	676	35	44.3	632	6	ABR68158	Human aec
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605	35	44.3	340	9	ADW46622	Adw46622	Salmonid	678	35	44.3	632	6	ABU96211	Novel hum
606	35	44.3	340	9	ADW46651	Adw46651	Salmonid	679	35	44.3	632	6	ABU92642	Human aec
607	35	44.3	340	9	ADW22678	Adw22678	Sleeping	680	35	44.3	632	6	ABO08719	Human sec
608	35	44.3	340	9	ADW03280	Adw03280	Sleeping	681	35	44.3	632	6	ABO02771	Human sec

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683	35	44.3	632	6	ABR94687	Human sec	756
684	35	44.3	632	6	ABU13918	Human PRO	757
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686	35	44.3	632	6	ABU98820	Novel hum	759
687	35	44.3	632	6	ABU98035	Novel hum	760
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690	35	44.3	632	6	ABU86275	Human sec	763
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693	35	44.3	632	6	ABU72503	Novel hum	766
694	35	44.3	632	6	ABU90895	Novel hum	767
695	35	44.3	632	6	ABO33954	Human sec	768
696	35	44.3	632	6	ABR99434	Human sec	769
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699	35	44.3	632	6	ABR92247	Human sec	772
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701	35	44.3	632	6	ABR78309	Human sec	774
702	35	44.3	632	6	ABU71971	Novel hum	775
703	35	44.3	632	6	ABU85045	Novel hum	776
704	35	44.3	632	6	ABO00184	Novel hum	777
705	35	44.3	632	6	ABO11516	Human sec	778
706	35	44.3	632	6	ABO02161	Human sec	779
707	35	44.3	632	6	ABU88735	Novel hum	780
708	35	44.3	632	6	ABU83430	Human sec	781
709	35	44.3	632	6	ABO06231	Novel hum	782
710	35	44.3	632	6	ABR59267	Human sec	783
711	35	44.3	632	6	ABO09329	Human sec	784
712	35	44.3	632	6	ABO19193	Novel hum	785
713	35	44.3	632	6	ABO11211	Human sec	786
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715	35	44.3	632	6	ABO16042	Human sec	788
716	35	44.3	632	6	ABO13748	Human sec	789
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718	35	44.3	632	6	ABU65651	Human sec	791
719	35	44.3	632	6	ABO07499	Human PRO	792
720	35	44.3	632	6	ABO03686	Human sec	793
721	35	44.3	632	6	ABR67134	Human sec	794
722	35	44.3	632	6	ABO15737	Human sec	795
723	35	44.3	632	6	ABU56018	Human sec	796
724	35	44.3	632	6	ABU72306	Human PRO	797
725	35	44.3	632	6	ABU65346	Human PRO	798
726	35	44.3	632	6	ABU95291	Novel hum	799
727	35	44.3	632	6	ABU71194	Human PRO	800
728	35	44.3	632	6	ABO07804	Human PRO	801
729	35	44.3	632	6	ABR70045	Human sec	802
730	35	44.3	632	6	ABR69378	Human sec	803
731	35	44.3	632	6	ABO01519	Human PRO	804
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733	35	44.3	632	6	ABR60118	Human sec	806
734	35	44.3	632	6	ABU90979	Human sec	807
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737	35	44.3	632	6	ABR68463	Human sec	810
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739	35	44.3	632	6	ABU85355	Human PRO	812
740	35	44.3	632	6	ABU83045	Human sec	813
741	35	44.3	632	6	ABU83125	Human sec	814
742	35	44.3	632	6	ABU94981	Novel hum	815
743	35	44.3	632	6	ABU90529	Novel hum	816
744	35	44.3	632	6	ABU84040	Human sec	817
745	35	44.3	632	6	ABU93691	Novel hum	818
746	35	44.3	632	6	ABO25949	Human PRO	819
747	35	44.3	632	6	ABR64936	Human sec	820
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752	35	44.3	632	6	ABR99129	Human sec	825
753	35	44.3	632	6	ABU57013	Human PRO	826
754	35	44.3	632	6	ABU85965	Novel hum	827

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ABU83735	Human sec	632	6	ABU83735
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ABU99854	Novel hum	632	6	ABU99854
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ABR90942	Human sec	632	6	ABR90942
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886	35	44.3	632	6	ABM10409	Human	sec	Abm10409	Human	sec	959	35	44.3	632	6	ABO38314	Human	PRO	AbO38314	Human	PRO
887	35	44.3	632	6	ABM11934	Human	sec	Abm11934	Human	sec	960	35	44.3	632	6	ABO45614	Human	PRO	AbO45614	Human	PRO
888	35	44.3	632	6	ABO52080	Human	PRO	AbO52080	Human	PRO	961	35	44.3	632	6	ABM20538	Human	sec	Abm20538	Human	sec
889	35	44.3	632	6	ABO52385	Human	PRO	AbO52385	Human	PRO	962	35	44.3	632	6	ADAB1437	Human	sec	AdAB1437	Human	sec
890	35	44.3	632	6	ADA19902	Novel	Hum	AdA19902	Novel	Hum	963	35	44.3	632	6	ABO16652	Human	sec	AbO16652	Human	sec
891	35	44.3	632	6	ABO23703	Human	sec	AbO23703	Human	sec	964	35	44.3	632	6	ABO18278	Human	sec	AbO18278	Human	sec
892	35	44.3	632	6	ADB17285	Human	tra	AdB17285	Human	tra	965	35	44.3	632	6	ABO22705	Human	PRO	AbO22705	Human	PRO
893	35	44.3	632	6	ADA17747	Human	PRO	AdA17747	Human	PRO	966	35	44.3	632	6	ABR23010	Human	PRO	AbR23010	Human	PRO
894	35	44.3	632	6	ABR97189	Human	sec	AbR97189	Human	sec	967	35	44.3	632	6	ABR92552	Human	sec	AbR92552	Human	sec
895	35	44.3	632	6	ABR86977	Human	sec	AbR86977	Human	sec	968	35	44.3	632	6	ABR81509	Human	sec	AbR81509	Human	sec
896	35	44.3	632	6	ABM11019	Human	sec	Abm11019	Human	sec	969	35	44.3	632	6	ABM77933	Human	sec	Abm77933	Human	sec
897	35	44.3	632	6	ABM28163	Human	sec	Abm28163	Human	sec	970	35									

974 35 44.3 632 6 ABO30332 Human sec
975 35 44.3 632 6 ABM07359 Human sec
976 35 44.3 632 6 ABM03950 Human sec
977 35 44.3 632 6 ABO37094 Human sec
978 35 44.3 632 6 ABO41669 Human sec
979 35 44.3 632 6 ABO35264 Human PRO
980 35 44.3 632 6 ABO25113 Human sec
981 35 44.3 632 6 ABO47505 Human sec
982 35 44.3 632 6 ABO47810 Human sec
983 35 44.3 632 6 ABO48420 Human sec
984 35 44.3 632 6 ABO51470 Human PRO
985 35 44.3 632 6 ABO51775 Human PRO
986 35 44.3 632 6 ABO50555 Human sec
987 35 44.3 632 6 ABR79679 Human sec
988 35 44.3 632 6 ABO16941 Human sec
989 35 44.3 632 6 ABO17973 Human sec
990 35 44.3 632 6 ABO20925 Human sec
991 35 44.3 632 6 ABR96884 Human sec
992 35 44.3 632 6 ADA38660 Human sec
993 35 44.3 632 6 ABM12239 Human sec
994 35 44.3 632 6 ABM16331 Human sec
995 35 44.3 632 6 ABM24198 Human sec
996 35 44.3 632 6 ABM14679 Human sec
997 35 44.3 632 6 ABM04560 Human sec
998 35 44.3 632 6 ABM06749 Human sec
999 35 44.3 632 6 ABM09189 Human sec
1000 35 44.3 632 6 ABO39229 Human sec

ALIGNMENTS

RESULT 1
ID ABR61469 standard; peptide; 15 AA.
XX ABR61469;
AC
XX
DT 01-SEP-2003 (first entry)
XX
DE Human disease specific marker CENP-E peptide.
XX
KW Human, biopolymer marker; disease state; Alzheimer's disease.
XX
OS Homo sapiens.
XX
XX WO2003045992-A1.
XX
XX 05-JUN-2003.
XX
XX 31-OCT-2002; 2002WO-CA001646.
XX
XX 23-NOV-2001; 2001US-009933399.
XX
XX (SYN-) SYN.X PHARMA INC.
XX
XX Jackowski G, Marshall J;
XX
XX WPI; 2003-505186/47.
XX
XX New biopolymer marker, useful for indicating, determining risk-assessment
XX of, or identifying therapeutic avenues related to, a disease state e.g.,
XX Alzheimer's disease.
XX
XX Claim 1; Page 41; 44pp; English.
XX
XX The invention relates to a novel biopolymer marker comprising a sequence
XX having 13 amino acids or its analyte, useful in indicating at least one
XX particular disease state. The biopolymer marker is useful for indicating,
XX determining risk-assessment of, or identifying therapeutic avenues
XX related to, a disease state e.g., Alzheimer's disease. The present
XX sequence represents the biopolymer marker of the invention

SQ Sequence 15 AA;
Query Match 100.0%; Score 79; DB 6; Length 15;
Best Local Similarity 100.0%; Pred. No. 5.9e-07;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 RHYGETKNNQRRSSRS 15
DB 1 RHYGETKNNQRRSSRS 15
|||||
RESULT 2
ID ADG89869 standard; protein; 355 AA.
XX
AC ADG89869;
XX
DT 11-MAR-2004 (first entry)
XX
DE Human kinesin motor protein CENP-E340 SEQ ID NO:4.
XX
KW human; CENP-E; HsCENP-E; kinesin motor protein; CENP-E340; cytostatic;
KW neuroprotective; gene therapy; cellular proliferation disorder; cancer;
KW neurological disorder; vesicular transport disorder;
KW hyperproliferative cell growth disorder; centromere-associated protein.
XX
XX Homo sapiens.
XX
XX WO2003104426-A2.
XX
XX 18-DEC-2003.
XX
XX 09-JUN-2003; 2003WO-US018203.
XX
XX 10-JUN-2002; 2002US-0387403P.
XX
XX (MERI) MERCK & CO INC.
XX
XX Harvey DM, Yang Y, Kohl NE;
XX
XX WPI; 2004-062347/06.
XX
XX N-PSDB; ADG89868.
XX
XX New centromere-associated motor protein, HsCENP-E, useful in diagnosing,
XX treating and preventing disorders characterized by excessive cellular
XX proliferation, including cancer, neurological disorders and disorders of
XX vesicular transport.
XX
XX Disclosure; SEQ ID NO 4; 108pp; English.
XX
XX The present sequence represents a human CENP-E (I) (HsCENP-E) which is a
XX kinesin motor protein, and a centromere-associated protein. The present
XX sequence is more specifically designated CENP-E340. Also described: (1) a
XX composition comprising (I) and a pharmaceutical excipient; (2) a method
XX for screening a compound as an agonist or antagonist of (I); (3) an
XX isolated and purified polynucleotide encoding (I), or which hybridises to
XX (I); (4) a method of detecting polynucleotide; (5) an expression vector
XX comprising the polynucleotide of (3); (6) a host cell comprising the
XX expression vector of (5); (7) a method for producing a polypeptide; (8) a
XX method of modulating cellular proliferation in a mammal; (9) a method of
XX inhibiting HsCENP-E mediated/induced cellular proliferation of a cell in
XX culture; and (10) a method of detecting the presence of cancer in an
XX individual. (1) has cytostatic and neuroprotective activities, and can be
XX used in gene therapy. The HsCENP-E protein can be used in screening
XX assays, in predictive medicine, e.g. diagnostic assays and
XX pharmacogenetics and in treating and preventing disorders characterised
XX by excessive cellular proliferation, including cancer, neurological
XX disorders and disorders of vesicular transport or useful in suppressing
XX hyperproliferative cell growth disorder.
XX
XX Sequence 355 AA;
Query Match 100.0%; Score 79; DB 8; Length 355;

Best Local Similarity 100.0%; Pred. No. 1.9e-05; Mismatches 0; Indels 0; Gaps 0;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RHYGETKNQSSRS 15
| | | | | | | | | | | | | | | |
Db 189 RHYGETKNQSSRS 203

RESULT 3
ADV50412
ID ADV50412 standard; protein; 355 AA.
XX AC
XX ADV50412;
XX DT 10-MAR-2005 (first entry)
XX DE Human CENP-E kinesin motor domain.
XX KW ATPase modulator; CENP-E; kinesin; cell proliferation;
KW hyperproliferative disorders; cancer; breast tumor; restenosis;
KW cardiovascular disease; autoimmune disease; immune disorder; arthritis;
KW inflammation; musculoskeletal disease; graft rejection;
KW inflammatory bowel disease; gastrointestinal disease; cytostatic;
KW vasotropic; immunosuppressive; antiarthritic; antiinflammatory;
KW gastrointestinal-gen.
XX KW
OS Homo sapiens.
XX KW
XX PN WO2004109290-A2.
XX PD 16-DEC-2004.
XX PF 28-MAY-2004; 2004WO-US017234.
XX PR 30-MAY-2003; 2003US-0474488P.
PR 03-JUN-2003; 2003US-0475873P.
PR 17-MAR-2004; 2004US-0553838P.
XX (ROSE-) ROSETTA INPHARMATICS LLC.
PA (MERI) MERCK & CO INC.
XX MAO M, Linsley PS, Buser CA, Marshall CG, Kim AS;
XX WPI; 2005-057663/06.
XX
XX Screening for modulators of target protein e.g., kinesin family 14
PT protein, by contacting target protein with candidate agent, and
PT determining whether candidate agent modulates activity of target protein.
XX
XX Example 7; SEQ ID NO 19; 118pp; English.
XX
XX The invention relates to a method (M1) of screening for modulators of a
CC target protein. The method involves contacting the target protein with
CC candidate agent, and determining whether the candidate agent modulates
CC activity of target protein, where the target protein comprises a sequence
CC that has more than 80% amino acid sequence identity to a fully defined
CC kinesin family 14 (Kif14) protein (SEQ ID No:2) or the Kif14 motor domain
CC sequence (SEQ ID No:3). Also described are: a method (M2) for modulating
CC cell proliferation, a method (M3) for treating a subject with a cellular
CC hyperproliferation disorder, a method (M4) for identifying candidate
CC subjects for treatment with an inhibitor of the activity of a target
CC protein, and a kit for screening for modulators of a target protein. A
CC cell viability assay, cell morphology assay, cell proliferation assay,
CC cell cycle distribution assay or apoptosis assay is used for determining
CC whether the candidate agent modulates the activity of the target protein.
CC The target protein comprises SEQ ID No:2, SEQ ID No:3, or a fragment of
CC SEQ ID No:3 having ATPase activity. The modulator is an inhibitor such as
CC RNA inhibitor, which is a Kif14 RNA inhibitor. The Kif14 RNA inhibitor
CC comprises sequences such as those disclosed in SEQ ID Nos 8, 9 or 23.
CC Method (M1) is useful for screening for modulators of a target protein,
CC particularly for screening modulators of Kif14 or Kif14 motor domain.
CC Method (M2) is useful for treating a subject with a cellular
CC hyperproliferation disorder such as cancer, preferably breast cancer.

CC Method (M3) is useful for treating restenosis, autoimmune disease,
CC arthritis, graft rejection or inflammatory bowel disease. This sequence
CC represents human CENP-E kinesin motor domain.
XX
SQ Sequence 355 AA;
Query Match 100.0%; Score 79; DB 9; Length 355;
Best Local Similarity 100.0%; Pred. No. 1.9e-05;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RHYGETKNQSSRS 15
| | | | | | | | | | | | | | | |
Db 189 RHYGETKNQSSRS 203

RESULT 4
ADG89867
ID ADG89867 standard; protein; 496 AA.
XX AC ADG89867;
XX DT 11-MAR-2004 (first entry)
XX DE Human kinesin motor protein CENP-E465 SEQ ID NO:2.
XX KW human; CENP-E; HsCENP-E; kinesin motor protein; CENP-E465; cytostatic;
KW neuroprotective; gene therapy; cellular proliferation disorder; cancer;
KW neurological disorder; vesicular transport disorder;
KW hyperproliferative cell growth disorder; centromere-associated protein.
XX OS Homo sapiens.
XX PN WO2003104426-A2.
XX PD 18-DEC-2003.
XX PF 09-JUN-2003; 2003WO-US018203.
XX PR 10-JUN-2002; 2002US-0387403P.
XX PA (MERI) MERCK & CO INC.
XX PI Harvey DM, Yang Y, Kohl NE;
XX WPI; 2004-062347/06.
XX N-PSDB; ADG89866.
XX New centromere-associated motor protein, HsCENP-E, useful in diagnosing,
PT treating and preventing disorders characterized by excessive cellular
PT proliferation, including cancer, neurological disorders and disorders of
PT vesicular transport.
XX
XX Claim 1; SEQ ID NO 2; 108pp; English.
XX
XX The present sequence represents a human CENP-E (I) (HsCENP-E) which is a
CC kinesin motor protein, and a centromere-associated protein. The present
CC sequence is more specifically designated CENP-E465. Also described: (1) a
CC composition comprising (1) and a pharmaceutical excipient; (2) a method
CC for screening a compound as an agonist or antagonist of (1); (3) an
CC isolated and purified polynucleotide encoding (1), or which hybridises to
CC (1); (4) a method of detecting polynucleotide; (5) an expression vector
CC comprising the polynucleotide of (3); (6) a host cell comprising the
CC expression vector of (5); (7) a method for producing a polypeptide; (8) a
CC method of modulating cellular proliferation in a mammal; (9) a method of
CC inhibiting HsCENP-E mediated/induced cellular proliferation of a cell in
CC culture; and (10) a method of detecting the presence of cancer in an
CC individual. (1) has cytostatic and neuroprotective activities, and can be
CC used in gene therapy. The HsCENP-E protein can be used in screening
CC assays, in predictive medicine, e.g. diagnostic assays and
CC pharmacogenetics and in treating and preventing disorders characterised
CC by excessive cellular proliferation, including cancer, neurological
CC disorders and disorders of vesicular transport or useful in suppressing
CC hyperproliferative cell growth disorder.

XX Sequence 496 AA;
SQ Query Match 100.0%; Score 79; DB 8; Length 496;
Best Local Similarity 100.0%; Pred. No. 2.7e-05; Indels 0; Gaps 0;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 RHYGETKNQSRSS 15
Db 189 RHYGETKNQSRSS 203
RESULT 5
ADW44257
ID ADW44257 standard; protein; 2503 AA.
XX ADW44257;
AC ADW44257;
XX 24-MAR-2005 (first entry)
DT Human centromere protein E variant 4 (CENPEV4).
DE
XX Drug screening; cell proliferation; proliferative disorder; cancer;
KW neoplasm; scleroderma; rheumatoid arthritis; musculoskeletal disease;
KW immune disorder; inflammation; cytostatic; dermatological; antiarthritic;
KW antirheumatic; centromere protein E; CENPE.
XX Homo sapiens.
OS
XX US2005003402-A1.
PN
XX 06-JAN-2005.
PD
XX 21-APR-2004; 2004US-00828985.
PF
XX 23-APR-2003; 2003US-0464905P.
PR 10-OCT-2003; 2003US-0510701P.
XX (ARMO//) ARMOUR C D.
PA (CAST//) CASTLE J C.
PA (GARR//) GARRETT-ENGELE P W.
PA (KANZ//) KAN Z.
PA (LOER//) LOERCH P M.
PA (TSIN//) TSINOREMAS N F.
XX Armour CD, Castle JC, Garrett-Englele PW, Kan Z, Loerch PM;
PI Tsinoemas NF;
PI WPI; 2005-065233/07.
XX N-PSDB; ADW44256.
DR
XX New nucleic acid encoding centromere protein E, useful for detecting
PT cancer and for inhibiting abnormal cell growth.
XX Example 4; SEQ ID NO 11; 55pp; English.
PS
XX The invention relates to a novel splice isoform of human centromere
CC protein E (CENPE) designated CENPE variant 2 (CENPEV2, ADW44253) and to a
CC nucleic acid encoding it. Compared to CENPEV1 (REFSEQ NM 001813,
CC NP_001804), the CENPEV2 isoform lacks the sequence encoded by exon 38
CC (residues 1972-2066 of CENPEV1) and also has an Ala at position 300
CC instead of Pro. The invention also relates to an expression vector
CC comprising the CENPEV2 nucleic acid operably linked to an exogenous
CC promoter, and a method of screening for a compound able to bind to or
CC interact with CENPEV2 or a fragment thereof. The invention also discloses
CC other splice variants of CENPE designated CENPEV3 (lacking residues
CC encoded by exons 17 and 38 relative to CENPEV1) and CENPEV4 (lacking
CC residues encoded by exons 17, 18 and 38 relative to CENPEV1), and their
CC encoding nucleic acids. The CENPEV2 protein, nucleic acid and CENPEV2-
CC interacting compounds are useful in methods for inhibiting abnormal cell
CC proliferation and for detecting, treating or preventing cancer. As CENPE
CC has also been implicated in rheumatic disorders, CENPEV2-interacting
CC compounds may also be useful in treating or preventing disorders such as

CC systemic sclerosis and rheumatoid arthritis. The present sequence
CC represents the human CENPEV4 protein.
XX
SQ Sequence 2503 AA;
Query Match 100.0%; Score 79; DB 9; Length 2503;
Best Local Similarity 100.0%; Pred. No. 0.00016; Indels 0; Gaps 0;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 RHYGETKNQSRSS 15
Db 189 RHYGETKNQSRSS 203
RESULT 6
ADW44255
ID ADW44255 standard; protein; 2543 AA.
XX ADW44255;
AC ADW44255;
XX 24-MAR-2005 (first entry)
DT Human centromere protein E variant 3 (CENPEV3).
DE
XX Drug screening; cell proliferation; proliferative disorder; cancer;
KW neoplasm; scleroderma; rheumatoid arthritis; musculoskeletal disease;
KW immune disorder; inflammation; cytostatic; dermatological; antiarthritic;
KW antirheumatic; centromere protein E; CENPE.
XX Homo sapiens.
OS
XX US2005003402-A1.
PN
XX 06-JAN-2005.
PD
XX 21-APR-2004; 2004US-00828985.
PF
XX 23-APR-2003; 2003US-0464905P.
PR 10-OCT-2003; 2003US-0510701P.
XX (ARMO//) ARMOUR C D.
PA (CAST//) CASTLE J C.
PA (GARR//) GARRETT-ENGELE P W.
PA (KANZ//) KAN Z.
PA (LOER//) LOERCH P M.
PA (TSIN//) TSINOREMAS N F.
XX Armour CD, Castle JC, Garrett-Englele PW, Kan Z, Loerch PM;
PI Tsinoemas NF;
PI WPI; 2005-065233/07.
XX N-PSDB; ADW44254.
DR
XX New nucleic acid encoding centromere protein E, useful for detecting
PT cancer and for inhibiting abnormal cell growth.
XX Example 4; SEQ ID NO 9; 55pp; English.
PS
XX The invention relates to a novel splice isoform of human centromere
CC protein E (CENPE) designated CENPE variant 2 (CENPEV2, ADW44253) and to a
CC nucleic acid encoding it. Compared to CENPEV1 (REFSEQ NM 001813,
CC NP_001804), the CENPEV2 isoform lacks the sequence encoded by exon 38
CC (residues 1972-2066 of CENPEV1) and also has an Ala at position 300
CC instead of Pro. The invention also relates to an expression vector
CC comprising the CENPEV2 nucleic acid operably linked to an exogenous
CC promoter, and a method of screening for a compound able to bind to or
CC interact with CENPEV2 or a fragment thereof. The invention also discloses
CC other splice variants of CENPE designated CENPEV3 (lacking residues
CC encoded by exons 17 and 38 relative to CENPEV1) and CENPEV4 (lacking
CC residues encoded by exons 17, 18 and 38 relative to CENPEV1), and their
CC encoding nucleic acids. The CENPEV2 protein, nucleic acid and CENPEV2-
CC interacting compounds are useful in methods for inhibiting abnormal cell
CC proliferation and for detecting, treating or preventing cancer. As CENPE
CC has also been implicated in rheumatic disorders, CENPEV2-interacting
CC compounds may also be useful in treating or preventing disorders such as

CC has also been implicated in rheumatic disorders, CENPEV2-interacting
 CC compounds may also be useful in treating or preventing disorders such as
 CC systemic sclerosis and rheumatoid arthritis. The present sequence
 CC represents the human CENPEV3 protein.

XX Sequence 2543 AA;
 SQ Query Match 100.0%; Score 79; DB 9; Length 2543;
 Best Local Similarity 100.0%; Pred. No. 0.00016;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RHYGETKNQSSRS 15
 |||||
 Db 189 RHYGETKNQSSRS 203

RESULT 7
 ADW44253
 ID ADW44253 standard; protein; 2568 AA.
 XX AC ADW44253;
 XX DT 24-MAR-2005 (first entry)
 XX DE Human centromere protein E variant 2 (CENPEV2).
 XX KW Drug screening; cell proliferation; proliferative disorder; cancer;
 KW neoplasm; scleroderma; rheumatoid arthritis; musculoskeletal disease;
 KW immune disorder; inflammation; cytostatic; dermatological; antiarthritic;
 KW antirheumatic; centromere protein E; CENPE.
 XX OS Homo sapiens.
 XX FH Key Location/Qualifiers
 FT Misc-difference 1971..1972
 FT /note= "These residues correspond to the exon 37-exon 39
 FT junction. The corresponding residues in CENPEV1 (residues
 FT 1971 and 2067) are separated by 95 amino acids encoded by
 FT exon 38 (SEQ ID NO:19)"
 XX US2005003402-A1.
 PN 06-JAN-2005.
 PD 21-APR-2004; 2004US-00828985.
 XX 23-APR-2003; 2003US-0464905P.
 PR 10-OCT-2003; 2003US-0510701P.
 XX (ARMO/) ARMOUR C D.
 PA (CAST/) CASTLE J C.
 PA (GARR/) GARRETT-ENGELE P W.
 PA (KANZ/) KAN Z.
 PA (LOER/) LOERCH P M.
 PA (TSIN/) TSINOREMAS N F.
 XX Armour CD, Castle JC, Garrett-Engle PW, Kan Z, Loerch PM;
 PI Tsinoremas NF;
 XX WPI: 2005-065233/07.
 DR N-PSDB; ADW44252.
 XX New nucleic acid encoding centromere protein E, useful for detecting
 PT cancer and for inhibiting abnormal cell growth.
 PS Claim 4; SEQ ID NO 7; 55pp; English.
 XX The invention relates to a novel splice isoform of human centromere
 CC protein E (CENPE) designated CENPE variant 2 (CENPEV2, ADW44253) and to a
 CC nucleic acid encoding it. Compared to CENPEV1 (REFSEQ NM 001813,
 CC NP 001804), the CENPEV2 isoform lacks the sequence encoded by exon 38
 CC (residues 1972-2066 of CENPEV1) and also has an Ala at position 300
 CC instead of Pro. The invention also relates to an expression vector

CC comprising the CENPEV2 nucleic acid operably linked to an exogenous
 CC promoter, and a method of screening for a compound able to bind to or
 CC interact with CENPEV2 or a fragment thereof. The invention also discloses
 CC other splice variants of CENPE designated CENPEV3 (lacking residues
 CC encoded by exons 17 and 38 relative to CENPEV1) and CENPEV4 (lacking
 CC residues encoded by exons 17, 18 and 38 relative to CENPEV1), and their
 CC encoding nucleic acids. The CENPEV2 protein, nucleic acid and CENPEV2-
 CC interacting compounds are useful in methods for inhibiting abnormal cell
 CC proliferation and for detecting, treating or preventing cancer. As CENPE
 CC has also been implicated in rheumatic disorders, CENPEV2-interacting
 CC compounds may also be useful in treating or preventing disorders such as
 CC systemic sclerosis and rheumatoid arthritis. The present sequence
 CC represents the specifically claimed human CENPEV2 protein.

XX Sequence 2568 AA;
 SQ Query Match 100.0%; Score 79; DB 9; Length 2568;
 Best Local Similarity 100.0%; Pred. No. 0.00016;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RHYGETKNQSSRS 15
 |||||
 Db 189 RHYGETKNQSSRS 203

RESULT 8
 ABG06505
 ID ABG06505 standard; protein; 2633 AA.
 XX AC ABG06505;
 XX DT 13-FEB-2002 (first entry)
 XX DE Novel human diagnostic protein #6496.
 XX KW Human; chromosome mapping; gene mapping; gene therapy; forensic;
 KW food supplement; medical imaging; diagnostic; genetic disorder.
 XX OS Homo sapiens.
 XX WO200175067-A2.
 PN 11-OCT-2001.
 PD 30-MAR-2001; 2001WO-US008631.
 XX 31-MAR-2000; 2000US-00540217.
 PR 23-AUG-2000; 2000US-00649167.
 XX (HYSE-) HYSEQ INC.
 PA Drmanac RT, Liu C, Tang YT;
 XX WPI: 2001-639362/73.
 DR N-PSDB; AAS70692.
 XX New isolated polynucleotide and encoded polypeptides, useful in
 PT diagnostics, forensics, gene mapping, identification of mutations
 PT responsible for genetic disorders or other traits and to assess
 PT biodiversity.
 XX Claim 20; SEQ ID NO 36864; 103pp; English.
 PS The invention relates to isolated polynucleotide (I) and polypeptide (II)
 CC sequences. (I) is useful as hybridisation probes, polymerase chain
 CC reaction (PCR) primers, oligomers, and for chromosome and gene mapping,
 CC and in recombinant production of (II). The polynucleotides are also used
 CC in diagnostics as expressed sequence tags for identifying expressed
 CC genes. (I) is useful in gene therapy techniques to restore normal
 CC activity of (II) or to treat disease states involving (II). (II) is
 CC useful for generating antibodies against it, detecting or quantitating a
 CC polypeptide in tissue, as molecular weight markers and as a food
 CC supplement. (II) and its binding partners are useful in medical imaging

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CC of sites expressing (II). (I) and (II) are useful for treating disorders
 CC involving aberrant protein expression or biological activity. The
 CC polypeptide and polynucleotide sequences have applications in
 CC diagnostics, forensics, gene mapping, identification of mutations
 CC responsible for genetic disorders or other traits to assess biodiversity
 CC and to produce other types of data and products dependent on DNA and
 CC amino acid sequences. ABG00010-ABG30377 represent novel human diagnostic
 CC amino acid sequences of the invention. Note: The sequence data for this
 CC patent did not appear in the printed specification, but was obtained in
 CC electronic format directly from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 CC
 XX SQ Sequence 2633 AA;
 Query Match 100.0%; Score 79; DB 4; Length 2633;
 Best Local Similarity 100.0%; Pred. No. 0.00017;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 RHYGETKMNQSRSS 15
 |||||
 Db 189 RHYGETKMNQSRSS 203
 |||||
 RESULT 9
 AAM39097
 ID AAM39097 standard; protein; 2663 AA.
 AC AAM39097;
 DT 22-OCT-2001 (first entry)
 XX Human polypeptide SEQ ID NO 2242.
 XX Human; neurotropic; immunosuppressant; cytostatic; gene therapy; cancer;
 KW peripheral nervous system; neuropathy; central nervous system; CNS;
 KW Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic;
 KW amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic;
 KW chemokinetic; thrombolytic; drug screening; arthritis; inflammation;
 KW leukaemia.
 OS Homo sapiens.
 XX WO200153312-A1.
 PN 26-JUL-2001.
 XX 26-DEC-2000; 2000WO-US034263.
 XX 23-DEC-1999; 99US-00471275.
 PR 21-JAN-2000; 2000US-00488725.
 PR 25-APR-2000; 2000US-00552317.
 PR 20-JUN-2000; 2000US-00598042.
 PR 19-JUL-2000; 2000US-00620312.
 PR 03-AUG-2000; 2000US-00653450.
 PR 14-SEP-2000; 2000US-00662191.
 PR 19-OCT-2000; 2000US-00693036.
 PR 29-NOV-2000; 2000US-00727344.
 XX (HYSE-) HYSEQ INC.
 XX Tang YT, Liu C, Asundi V, Chen R, Ma Y, Qian XB, Ren F, Wang D;
 PI Wang J, Wang Z, Wehrman T, Xu C, Xue AJ, Yang Y, Zhang J, Zhao QA;
 PI Zhou P, Goodrich R, Drmanac RT;
 XX WPI; 2001-442253/47.
 DR N-PSDB; AAI58253.
 XX Novel nucleic acids and polypeptides, useful for treating disorders such
 PT as central nervous system injuries.
 PT Example 4; SEQ ID NO 2242; 10078pp; English.
 PS The invention relates to human nucleic acids (AAI57798-AAI61369) and the

CC encoded polypeptides (AAM38642-AAM42213) with neurotropic,
 CC immunosuppressant and cytostatic activity. The polynucleotides are useful
 CC in gene therapy. A composition containing a polypeptide or polynucleotide
 CC of the invention may be used to treat diseases of the peripheral nervous
 CC system, such as peripheral nervous injuries, peripheral neuropathy and
 CC localised neuropathies and central nervous system diseases, such as
 CC Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic
 CC lateral sclerosis, and Shy-Drager Syndrome. Other uses include the
 CC utilisation of the activities such as: immune system suppression,
 CC activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic
 CC and thrombolytic activity, cancer diagnosis and therapy, drug screening,
 CC assays for receptor activity, arthritis and inflammation, leukaemias and
 CC C.N.S disorders. Note: The sequence data for this patent did not form
 CC part of the printed specification
 XX SQ Sequence 2663 AA;
 Query Match 100.0%; Score 79; DB 4; Length 2663;
 Best Local Similarity 100.0%; Pred. No. 0.00017;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 RHYGETKMNQSRSS 15
 |||||
 Db 189 RHYGETKMNQSRSS 203
 |||||
 RESULT 10
 ADQ17932
 ID ADQ17932 standard; protein; 2663 AA.
 AC ADQ17932;
 DT 26-AUG-2004 (first entry)
 XX Human soft tissue sarcoma-upregulated protein - SEQ ID 749.
 XX soft tissue sarcoma; cytostatic; gene therapy; vaccine; screening; human.
 KW Homo sapiens.
 OS WO2004048938-A2.
 PN 10-JUN-2004.
 XX 26-NOV-2003; 2003WO-US038193.
 XX 26-NOV-2002; 2002US-0429739P.
 XX (PROT-) PROTEIN DESIGN LABS INC.
 XX Aziz N, Ginsburg WM, Zlotnik A;
 PI WPI; 2004-441208/41.
 DR Early detection of soft tissue sarcoma comprises determining expression
 PT of a gene in a first soft tissue sample and a normal soft tissue sample
 PT and comparing the gene expression, also useful in treating soft tissue
 PT sarcoma.
 XX Example 2; SEQ ID NO 749; 210pp; English.
 XX The invention relates to a novel method for detecting soft tissue sarcoma
 CC which comprises obtaining a first soft tissue sample from an individual,
 CC and a normal soft tissue sample from the same or different individual,
 CC determining the expression of a gene in both samples and comparing the
 CC expression of the gene in the first soft tissue sample indicates the
 CC of protein expression in the first soft tissue sample indicates the
 CC presence of soft tissue sarcoma. The method of the invention has
 CC cytostatic applications and may be useful for detecting soft tissue
 CC sarcoma, possibly via gene therapy or vaccine production. The nucleic
 CC acid sequences may be useful in diagnostic and screening applications.
 CC The current sequence is that of a human soft tissue sarcoma-upregulated
 CC protein of the invention. The current sequence is not shown within the

CC specification per se but was submitted in CD format by the inventor.
XX Sequence 2663 AA;
SQ

Query Match 100.0%; Score 79; DB 8; Length 2663;
Best Local Similarity 100.0%; Pred. No. 0.00017;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RHYGETKNQSRSS 15
|||
DB 189 RHYGETKNQSRSS 203

RESULT 11
ADX06867
ID ADX06867 standard; protein; 2663 AA.
XX
AC ADX06867;
XX
DT 21-APR-2005 (first entry)
XX
DE Cyclin-dependent kinase modulation biomarker SEQ ID NO 1432.
XX
KW cytotstatic; cyclin-dependent kinase; cdk; biomarker.
XX
OS Homo sapiens.
XX
PN WO2005012875-A2.
XX
PD 10-FEB-2005.
XX
PF 29-JUL-2004; 2004WO-US024424.
XX
PR 29-JUL-2003; 2003US-0490890P.
XX
PA (BRIM) BRISTOL-MYERS SQUIBB CO.
XX
PI Li M, Rupnow BA, Webster KR, Jackson DG, Wong TW;
XX
DR WPI; 2005-163068/17.
DR N-PSDB; ADX06866.
XX

PT Biomarkers useful for predicting or determining the response of a mammal
PT to a cancer treatment comprising administration of a modulator of cyclin-
PT dependent kinase activity.

PS Claim 5; SEQ ID NO 1432; 141pp; English.

CC This invention describes a novel method of predicting or determining
CC whether a mammal will respond or is responding to an anti-cancer agent
CC that modulates cyclin-dependent kinase (cdk) activity. The method
CC comprises measuring the level of one or more biomarkers selected from
CC 2774 biomarkers given in the specification (nucleotide sequence SEQ ID
CC NO:1246 (Genbank EST W28729) is especially preferred). The method of the
CC invention is utilized in a kit for determining or predicting whether
CC patient would be susceptible or resistant to treatment by an agent
CC modulating cdk activity. The invention also describes a method for
CC utilizing individualized genetic profiles for treating diseases and
CC disorders based on patient's response and molecular level, specialized
CC microarrays comprising the biomarkers described, antibodies directed
CC against the biomarkers and a cell culture model to identify biomarkers.
CC The cdk modulator is preferably N-5-[[5-(1,1-Dimethylethyl)-2-
CC oxazoly]methyl]thiol-2-thiazolyl-4-piperidine carboxamide, 0.5-L-
CC tartaric acid salt. Note: The sequence data for this patent did not form
CC part of the printed specification, but was obtained in electronic format
CC directly from WIPO at ftp.wipo.int/pub/published_pct_sequences. This
CC sequence represents a biomarker used in the method of the invention.

SQ Sequence 2663 AA;

Query Match 100.0%; Score 79; DB 9; Length 2663;
Best Local Similarity 100.0%; Pred. No. 0.00017;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RHYGETKNQSRSS 15
|||
DB 189 RHYGETKNQSRSS 203

RESULT 12
AAM40883
ID AAM40883 standard; protein; 2688 AA.
XX
AC AAM40883;
XX
DT 22-OCT-2001 (first entry)
XX
DE Human polypeptide SEQ ID NO 5814.

XX
KW Human; nootropic; immunosuppressant; cytotstatic; gene therapy; cancer;
KW peripheral nervous system; neuropathy; central nervous system; CNS;
KW Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic;
KW amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic;
KW chemokinetic; thrombolytic; drug screening; arthritis; inflammation;
KW leukaemia.

XX
OS Homo sapiens.
XX
PN WO200153312-A1.
XX
PD 26-JUL-2001.

XX
PF 26-DEC-2000; 2000WO-US034263.

XX
PR 23-DEC-1999; 99US-00471275.
PR 21-JAN-2000; 2000US-00488725.
PR 25-APR-2000; 2000US-0052317.
PR 20-JUN-2000; 2000US-00598042.
PR 19-JUL-2000; 2000US-00620312.
PR 03-AUG-2000; 2000US-00653450.
PR 14-SEP-2000; 2000US-00662191.
PR 19-OCT-2000; 2000US-00693036.
PR 29-NOV-2000; 2000US-00727344.
XX
PA (HYSE-) HYSEQ INC.

XX
PI Tang YT, Liu C, Asundi V, Chen R, Ma Y, Qian XB, Ren P, Wang D;
PI Wang J, Wang Z, Wahrman T, Xu C, Xue AJ, Yang Y, Zhang J, Zhao QA;
PI Zhou P, Goodrich R, Drmanac RT;

XX
DR WPI; 2001-442253/47.
DR N-PSDB; AAI60039.

XX
PT Novel nucleic acids and polypeptides, useful for treating disorders such
PT as central nervous system injuries.

XX
PS Example 2; SEQ ID NO 5814; 10078pp; English.

CC The invention relates to human nucleic acids (AAI57798-AAI61369) and the
CC encoded polypeptides (AAM38642-AAM42213) with nootropic,
CC immunosuppressant and cytotstatic activity. The polynucleotides are useful
CC in gene therapy. A composition containing a polypeptide or polynucleotide
CC of the invention may be used to treat diseases of the peripheral nervous
CC system, such as peripheral nervous injuries, peripheral neuropathy and
CC localised neuropathies and central nervous system diseases, such as
CC Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic
CC lateral sclerosis, and Shy-Drager Syndrome. Other uses include the
CC utilisation of the activities such as: immune system suppression.
CC Activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic
CC and thrombolytic activity, cancer diagnosis and therapy, drug screening,
CC assays for receptor activity, arthritis and inflammation, leukaemia and
CC C.N.S disorders. Note: The sequence data for this patent did not form
CC part of the printed specification

XX
SQ Sequence 2688 AA;

Mon Apr 24 09:14:16 2006

Query Match 100.0%; Score 79; DB 4; Length 2688;
Best Local Similarity 100.0%; Pred. No. 0.00017;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RHYGETKNQSSRS 15
| | | | | | | | | | | | | | | |
DB 213 RHYGETKNQSSRS 227

RESULT 13
ID AAY01632 standard; protein; 2954 AA.
XX AAY01632;
XX 22-JUN-1999 (first entry)
XX Amino acid sequence of centromere-associated protein-E (CENP-E).
XX CENP-E; centromere-associated protein-E; ATPase activity;
KW plus end-directed microtubule motor activity; chromosome congression;
KW microtubule binding activity; chromosome movement; mitosis;
KW cell proliferation; tumor; metastasis; vascular malformation;
KW inflammatory disease; immune disease; angiogenesis; hypertension;
KW restenosis; fungal infection; selective herbicide; fungicide;
KW insecticide; plant growth regulator; activator; cancer cell marker.
XX Xenopus sp.
XX WO9913061-A1.
XX 18-MAR-1999.
XX 10-SEP-1998; 98WO-US019231.
XX 11-SEP-1997; 97US-0058645P.
XX (REGC) UNIV CALIFORNIA.
XX Wood KW, Sakowicz R, Goldstein LSB, Cleveland DW;
PI WPI; 1999-229233/19.
XX N-PSDB; AAX46819.
XX Centromere-associated protein-E and related nucleic acid.

Claim 5; Page 66-67; 77pp; English.
XX The present sequence represents CENP-E (centromere-associated protein-E)
XX of Xenopus. The protein has at least one of plus end-directed microtubule
CC motor activity, ATPase (adenosine triphosphatase) activity and
CC microtubule binding activity. CENP-E is the motor that powers chromosome
CC movement toward microtubule plus ends and is essential for congression of
CC chromosomes during mitosis. Modulators of CENP-E can thus control cell
CC proliferation. Agents that modulate CENP-E activity are lead therapeutic,
CC biocultural and diagnostic agents, e.g. for treatment of unwanted
CC cell proliferation (typical of many examples are tumors and metastases;
CC vascular malformation; inflammatory and immune diseases; angiogenesis;
CC hypertension; restenosis; and fungal infections), also as plant-
CC protection agents (selective herbicides, fungicides and insecticides) and
CC plant growth regulators or activators for improving yields. CENP-E is
CC also a diagnostic marker for dividing cells, including cancer cells
XX Sequence 2954 AA;
SQ

Query Match 87.3%; Score 69; DB 2; Length 2954;
Best Local Similarity 86.7%; Pred. No. 0.011;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 RHYGETKNQSSRS 15
| | | | | | | | | | | | | | | |
DB 187 RHYGETKNQSSRS 201

RESULT 14
ID ADX97061 standard; protein; 694 AA.
XX ADX97061;
XX 21-APR-2005 (first entry)
XX Plant full length insert polypeptide seqid 59725.

XX plant protectant; plant growth regulant; gene therapy; plant;
KW recombinant DNA construct; physical array; plant breeding marker;
KW cold tolerance; heat tolerance; drought tolerance; herbicide tolerance;
KW extreme osmotic condition; pathogen tolerance; pest tolerance;
KW growth rate; cell cycle pathway; disease resistance;
KW galactomannan production; lignin production; plant growth regulator;
KW yield; plant growth; plant development; seed oil; protein yield;
KW protein content.

XX Unidentified.
XX US2004034888-A1.
XX 19-FEB-2004.
XX 28-APR-2003; 2003US-00425114.
XX 06-MAY-1999; 99US-00304517.
XX 05-NOV-2001; 2001US-00985678.

XX (LIUJ/) LIU J.
XX (ZHOU/) ZHOU Y.
XX (KOVA/) KOVALIC D K.
XX (SCRE/) SCREEN S E.
XX (TABA/) TABASKA J E.
XX (CAOY/) CAO Y.

XX Liu J, Zhou Y, Kovalic DK, Screen SE, Tabaska JE, Cao Y;
PI WPI; 2004-180133/17.
XX New recombinant DNA construct, useful for improving plant tolerance to
XX cold, heat, drought, herbicides, extreme osmotic conditions, pathogens or
XX pests, for conferring increased resistance to plant disease, or for
XX improving yield.

XX Claim 1; SEQ ID NO 59725; 15pp; English.

XX The invention describes a recombinant DNA construct comprising a
XX polynucleotide consisting of a sequence encoding an amino acid sequence
XX available in electronic form from the US patent office at
XX ftp.segdata.uspto.gov/sequence.html?docID:2004034888. The polynucleotide
XX of the invention are also useful in physical arrays of molecules and as
XX plant breeding markers. The recombinant DNA construct is useful for
XX improving plant tolerance to cold, heat, drought, herbicides, extreme
XX osmotic conditions, pathogens or pests, for manipulating growth rate in
XX plant cells by modification of the cell cycle pathway, for conferring
XX increased resistance to plant disease, for increasing the rate of homologous
XX lignin or plant growth regulators, for improving the rate of modification of
XX recombination in plants, for improving yield by modification of
XX photosynthesis or carbohydrate, nitrogen or phosphorus use and/or uptake
XX or by providing improved plant growth and development under at least one
XX stress condition or for modifying seed oil or protein yield and/or
XX content. This is the amino acid sequence of a plant full length insert
XX polypeptide that can be used in the recombinant DNA construct of the
XX invention.

XX Sequence 694 AA;
SQ

Query Match 82.3%; Score 65; DB 8; Length 694;
Best Local Similarity 80.0%; Pred. No. 0.012;
Matches 12; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 RHYGETKNQRRSSRS 15
 DB 221 RHFGETNNRRSSRS 235

RESULT 15
 AAR57365
 ID AAR57365 standard; protein; 955 AA.
 XX AC AAR57365;
 XX DT 16-OCT-2003 (revised)
 XX DT 25-MAR-2003 (revised)
 XX DT 08-MAR-1995 (first entry)
 XX DE K39 polypeptide of Leishmania chagasi.
 XX KW Parasite; leishmaniasis; infection; repeat unit; vaccine; antigen;
 XX KW Leishmania chagasi.
 XX OS Leishmania donovani chagasi.
 XX PN WO9416331-A1.
 XX PD 21-JUL-1994.
 XX PF 10-JAN-1994; 94WO-US000324.
 XX PR 15-JAN-1993; 93US-00006676.
 XX PA (IASY-) IASYS CORP.
 XX PI Reed SG;
 XX DR WPI; 1994-249402/30.
 XX DR N-PSDB; RAQ70152.
 XX PT Diagnosis of Leishmaniasis - by determining the presence of antibodies
 XX PT that bind to a K39 repeat unit antigen.
 XX PS Disclosure; Page 12-15; 28pp; English.
 XX CC The K39 polypeptide comprises a number of repeated units (described in
 CC AAR57366). Detection of antibodies directed against this repeated unit in
 CC a patient's sample is indicative of leishmaniasis. The antigenic repeat
 CC unit can itself be used as a vaccine to protect against infection by a
 CC leishmania parasite. (Updated on 25-MAR-2003 to correct PN field.)
 CC (Updated on 16-OCT-2003 to standardise OS field)
 XX SQ Sequence 955 AA;

Query Match 68.4%; Score 54; DB 2; Length 955;
 Best Local Similarity 73.3%; Pred. No. 1.6;
 Matches 11; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 RHYGETKNQRRSSRS 15
 DB 241 RHTASTKNDRSSRS 255

RESULT 16
 AAW03691
 ID AAW03691 standard; protein; 955 AA.
 XX AC AAW03691;
 XX DT 16-OCT-2003 (revised)
 XX DT 09-MAR-1997 (first entry)
 XX DE Leishmania chagasi K39 antigen.
 XX KW Leishmania chagasi; acidic ribosomal antigen; LcP0; epitope; K39.

Query Match 68.4%; Score 54; DB 2; Length 955;
 Best Local Similarity 73.3%; Pred. No. 1.6;
 Matches 11; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

XX Leishmania donovani chagasi.
 XX WO9633414-A2.
 XX PD 24-OCT-1996.
 XX PF 19-APR-1996; 96WO-US005472.
 XX PR 21-APR-1995; 95US-00428414.
 XX PA (CORI-) CORIXA CORP.
 XX PI Reed SG;
 XX DR WPI; 1996-485984/48.
 XX DR N-PSDB; AAT42166.
 XX PT New Leishmania acidic ribosomal P-protein family polypeptide - used to
 PT develop prods. for diagnosis, detection and protection against Leishmania
 PT infections.
 XX PS Disclosure; Page 36-43; 76pp; English.
 XX CC Compounds including polypeptides that contain at least an epitope of the
 CC L. chagasi acidic ribosomal antigen LcP0 are useful in a variety of
 CC immunoassays for detecting Leishmania infection. Portions of LcP0
 CC (AAT42164) contg. at least the 17 C-terminal amino acids (AAT42165) have
 CC been found to generate a signal in an ELISA that is equivalent to that
 CC generated by the full length LcP0. A combination polypeptide may also be
 CC used, comprising an LcP0 epitope along with an epitope derived from the
 CC Leishmania K39 antigen (AAT42166), pref. the K39 repeat unit antigen
 CC having the sequence given in AAW03690. (Updated on 16-OCT-2003 to
 CC standardise OS field)
 XX SQ Sequence 955 AA;

Query Match 68.4%; Score 54; DB 2; Length 955;
 Best Local Similarity 73.3%; Pred. No. 1.6;
 Matches 11; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 RHYGETKNQRRSSRS 15
 DB 241 RHTASTKNDRSSRS 255

RESULT 17
 ABB62322
 ID ABB62322 standard; protein; 2013 AA.
 XX AC ABB62322;
 XX DT 26-MAR-2002 (first entry)
 XX DE Drosophila melanogaster polypeptide SEQ ID NO 13758.
 XX KW Drosophila; developmental biology; cell signalling; insecticide;
 XX KW pharmaceutical.
 XX OS Drosophila melanogaster.
 XX PN WO200171042-A2.
 XX PD 27-SEP-2001.
 XX PF 23-MAR-2001; 2001WO-US009231.
 XX PR 23-MAR-2000; 2000US-0191637P.
 XX PR 11-JUL-2000; 2000US-00614150.
 XX PA (PEKE) PE CORP NY.
 XX PI Venter JC, Adams M, Li PWD, Myers EW;

WPI; 2000-602362/57.
N-PSDB; AAC74870.

Novel nucleic acids and peptides derived from open reading frame X,
useful for treating e.g. cancers, proliferative disorders,
neurodegenerative disorders and cardiovascular disease.

Claim 11; Page 888-889; 5507pp; English.

AAC74446 to AAC77606 encode the proteins given in AAB40237 to AAB43397,
which represent the human ORFX open reading frames 1 to 3161. The ORFX
sequences have activities such as: cytostatic; hepatotropic; vulnery;
antipariatic; antiparkinsonian; nootropic; neuroprotective; osteopathic;
anticongulsant; antiarthritic; immunosuppressant; immunostimulant;
cardiant; thrombolytic; coagulant; vasotrophic; antidiabetic; hypotensive;
dermatological; immunosuppressive; antiinflammatory; antibacterial;
antiviral; antifungal; antineumatic; antithyroid; and antanaemic. The
sequences can be used for determining the presence of or predisposition
to, or preventing or treating pathological conditions associated with an
ORFX-associated disorder. The nucleic acids can be used to express ORFX
proteins in gene therapy vectors. The proteins and nucleic acids may be
used to treat cancers, proliferative disorders, neurodegenerative
disorders, osteoarthritis, graft vs host disease, cardiovascular disease,
diabetes mellitus, hypertension, hypothyroidism, cholesterol ester
storage, systemic lupus erythematosus, severe combined immunodeficiency
(SCID), AIDS, viral, bacterial or fungal infection, malaria, autoimmune
disorders, asthma, allergies, aplastic anaemia, burns, wounds, bone and
cartilage damage, nocturnal haemoglobinuria, antiinflammatory disease; to
enhance coagulation; to inhibit thrombosis; and as a contraceptive

Sequence 154 AA;

Query Match 65.8%; Score 52; DB 3; Length 154;
Best Local Similarity 66.7%; Pred. No. 0.49;
Matches 10; Conservative 2; Mismatches 3; Indels 0; Gaps 0

QY 1 RHYGETKMNQRSSRS 15
|||:::|||
Db 29 RHTGTQNEHSSRS 43

RESULT 19
ID BP31636
ABP31636 standard; protein; 154 AA.

XX AC ABP31636;
XX DT
XX DE Human structural protein-like ORF609 protein, SEQ ID NO:1218.
XX KW Human; ORF; open reading frame; ORFX; drug screening; diagnosis;
KW KW disease monitoring; cytokine; cell proliferation; cell differentiation;
KW KW immune modulation; haematopoiesis regulation; tissue growth;
KW KW angiogenesis; activin; inhibin; chemotactic; chemokinetic; haemostatic;
KW KW thrombolytic; tumour inhibition; bodily characteristic; fertility;
KW KW behaviour; cancer; proliferative disorder; neurological disorder;
KW KW cardiovascular disease; immune system disorder; organ transplantation;
KW KW tissue growth disorder; tissue regeneration disorder; diabetes mellitus;
KW KW hypothyroidism; cholesterol ester storage disease; infection; vulnery;
KW KW vasotrophic; antipariatic; antidiabetic; cyostatic; nootropic;
KW KW neuroprotective; antihypertensive; antithyroid; anticoagulant; thrombolytic;
KW KW cardiant; hypotensive; antithyroid; antiinflammatory; immunomodulator;
KW KW dermatological; analgesic; virucide; antibacterial; fungicide.

XX OS Homo sapiens.
XX XX
XX FN W0200190366-A2.
XX PD 29-NOV-2001.
XX PF 24-MAY-2001; 2001WO-US017076.

XX 24-MAY-2000; 2000US-0206690P.
 XX (CURA-) CURAGEN CORP.
 XX Leach MD, Shimkets RA;
 XX WPI; 2002-106200/14.
 XX N-PSDB; ABN75662.
 XX Novel human polypeptides and polynucleotides useful for diagnosing,
 PT preventing and treating cardiovascular disease, neurodegenerative,
 PT hyperproliferative disorders and disorders related to organ
 PT transplantation.
 XX Claim 10; Page 570; 2508pp; English.
 XX Sequences ABP31028-ABP3561 represent 4534 novel human proteins
 CC designated ORF (open reading frame) 1-4534, and sequences ABN75054-
 CC ABN79587 represent cDNAs encoding them. The invention also encompasses
 CC polypeptides at least 80% identical to the ORF1-ORF4534 (collectively
 CC referred to as ORFX) proteins, polynucleotides at least 85% identical to
 CC the ORFX nucleic acid sequences, vectors and host cells comprising ORFX
 CC polynucleotides, the recombinant production of ORFX proteins, antibodies
 CC specific for ORFX proteins, methods of detecting ORFX polynucleotides and
 CC polypeptides, methods of screening for modulators of ORFX expression or
 CC activity, and methods of screening individuals for a predisposition to an
 CC ORFX-associated disorder. The ORFX proteins of the invention have a wide
 CC range of biological activities, such as cytokine, cell proliferation,
 CC cell differentiation, immune modulation, haematopoiesis regulation,
 CC tissue growth, angiogenesis, activin or inhibin activity, chemotactic/
 CC chemokinetic activity, haemostatic activity, thrombolytic activity,
 CC receptor/ligand, antiinflammatory activity, tumour inhibition activity,
 CC and antiinfective activity, and may also be involved in the determination
 CC of bodily characteristics, fertility and behaviour. ORFX proteins,
 CC nucleic acids and antibodies may be used in the treatment of cancers,
 CC other proliferative disorders such as psoriasis and benign tumours,
 CC neurological disorders such as epilepsy and Alzheimer's disease,
 CC cardiovascular diseases, immune system disorders, disorders related to
 CC organ transplantation, disorders of tissue growth and regeneration,
 CC diseases such as diabetes mellitus, hypothyroidism, and cholesterol ester
 CC storage disease, and infectious diseases caused by viral, bacterial,
 CC fungal and other pathogens. ORFX nucleic acids may also be used as a
 CC source of primers and probes, in the detection of ORFX genomic sequences
 CC or transcripts, in the identification and cloning of homologous
 CC sequences, in genetic diagnosis, and in forensic biology. The ORFX
 CC nucleic acids may additionally be used to produce transgenic animals
 CC which may be useful for studying the function and/or activity of ORFX
 CC protein, and in drug screening. The ORFX proteins may also be used as
 CC immunogens to generate specific antibodies, which are useful in the
 CC diagnosis, treatment and monitoring of ORFX-associated diseases
 XX Sequence 154 AA;
 SQ Query Match 65.8%; Score 52; DB 5; Length 154;
 Best Local Similarity 66.7%; Pred. No. 0.49;
 Matches 10; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
 QY 1 RHYGETKNQRSSRS 15
 ||| |||: |||
 Db 29 RHTGTTQMNHSRS 43
 RESULT 20
 ABB80079
 ID ABB80079 standard; protein; 341 AA.
 XX AC ABB80079;
 XX 27-AUG-2002 (first entry)
 DT Human kinesin motor protein (HsKrp5) motor domain amino acid sequence.
 DE
 XX

KW Human; kinesin motor protein; HsKrp5; cytostatic; cardiovascular;
 KW immunomodulatory; anti-inflammatory; vaccine; gene therapy;
 KW spindle morphogenesis; chromosome; cell division;
 KW cellular proliferation disorder; cancer; hyperplasias; restenosis;
 KW cardiac hypertrophy; immune disorder; inflammation.
 XX Homo sapiens.
 XX US6379941-B1.
 XX 30-APR-2002.
 XX 27-NOV-2000; 2000US-00724517.
 XX 17-AUG-2000; 2000US-00641807.
 XX (CYTO-) CYTOKINETICS INC.
 XX Beraud C, Freedman R;
 XX WPI; 2002-413719/44.
 XX Isolated human Kinesin motor protein HsKrp5, useful for preventing,
 PT diagnosing and treating e.g. cancer, hyperplasias, restenosis, cardiac
 PT hypertrophy, immune disorders and inflammation.
 XX Claim 4; Fig 4; 29pp; English.
 XX The invention relates to an isolated human Kinesin motor protein
 CC (HsKrp5). The activity of the protein of the invention may be described
 CC as cytostatic, cardiovascular, immunomodulatory and anti-inflammatory.
 CC The protein may be used in a vaccine or in gene therapy. Kinesin-related
 CC proteins (KRPs) participate in spindle morphogenesis and chromosome
 CC movement in cell division. The anti-HsKrp5 agonists, antibodies and
 CC antagonists may be used to regulate HsKrp5 expression and activity. The
 CC anti-HsKrp5 antibodies may also be used as diagnostic agents for
 CC detecting the presence of HsKrp5 in samples (e.g. by enzyme linked
 CC immunosorbant assay (ELISA)) and therefore diagnose diseases associated
 CC with aberrant HsKrp5 expression and activity. They may be used in this
 CC way to prevent, diagnose and treat cellular proliferation disorders e.g.
 CC cancer, hyperplasias, restenosis, cardiac hypertrophy, immune disorders
 CC and inflammation. The current sequence represents the human kinesin motor
 CC protein (HsKrp5) motor domain amino acid sequence
 XX Sequence 341 AA;
 SQ Query Match 65.8%; Score 52; DB 5; Length 341;
 Best Local Similarity 66.7%; Pred. No. 1.2;
 Matches 10; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
 QY 1 RHYGETKNQRSSRS 15
 ||| |||: |||
 Db 192 RHTGTTQMNHSRS 206
 RESULT 21
 ABG72398
 ID ABG72398 standard; protein; 341 AA.
 XX AC ABG72398;
 XX 11-FEB-2003 (first entry)
 DT Human kinesin protein, HsKrp5, motor domain.
 DE
 XX Human; kinesin; HsKrp5; ATPase; microtubule; cellular proliferation;
 KW cancer; hyperplasia; restenosis; cardiac hypertrophy; autoimmune disease;
 KW immune disorder; arthritis; graft rejection; inflammatory bowel disease;
 KW inflammation; neurological disorder; vesicular transport disorder;
 KW enzyme; motor domain.
 XX Homo sapiens.
 XX

PN US6448026-B1.
 XX 10-SEP-2002.
 PD 27-NOV-2000; 2000US-00723096.
 XX 17-AUG-2000; 2000US-00641807.
 PF (CYTO-) CYTOKINETICS INC.
 XX Beraud C, Freedman R;
 PI WPI; 2003-089119/08.
 XX N-PSDB; ABX13614.
 DR Screening for modulators of human kinesin protein HsKrp5, which are
 XX useful in treating cancers or restenosis, comprises detecting binding or
 PT ATPase activity levels of the protein in a first and second concentration
 PT of a candidate agent.
 XX Claim 8; Fig 4; 30pp; English.
 PS The invention relates to screening for modulators of a target protein,
 XX comprises detecting the level of binding activity or ATPase activity of
 CC the target protein when contacted with a first and second concentration
 CC of a candidate agent. The target protein comprises a sequence that has
 CC greater than 90% amino acid identity with a sequence of human kinesin
 CC protein HsKrp5 (or its motor domain). The method is useful for screening
 CC for modulators of a target protein having microtubule stimulated ATPase
 CC activity, particularly the human kinesin protein HsKrp5. The modulators
 CC of HsKrp5 are useful in diagnosing, preventing or treating cellular
 CC proliferation (e.g. cancers (many examples given in the specification) or
 CC hyperplasia), restenosis, cardiac hypertrophy, autoimmune disease, immune
 CC disorders, arthritis, graft rejection, inflammatory bowel disease,
 CC inflammation, neurological disorders, or disorders of vesicular
 CC transport. The present sequence represents human HsKrp5, motor domain
 XX Sequence 341 AA;
 SQ Query Match 65.8%; Score 52; DB 6; Length 341;
 Best Local Similarity 66.7%; Pred. No. 1.2;
 Matches 10; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
 QY 1 RHYGETKMNQSRSS 15
 DB 192 RHTGTTQMNEHSRS 206
 RESULT 22
 ABR44339
 ID ABR44339 standard; protein; 348 AA.
 XX ABR44339;
 AC 11-AUG-2003 (first entry)
 DT Polypeptide-kinesin-38.28.
 DE Polypeptide-kinesin-38.28;
 XX paralytic; arrhythmia; bronchial asthma;
 KW peptic ulcer.
 KW Unidentified.
 OS CN1380331-A.
 XX 20-NOV-2002.
 PD 10-APR-2001; 2001CN-00105929.
 PF 10-APR-2001; 2001CN-00105929.
 XX (SHAN-) SHANGHAI BIONOW GENE DEV INC.
 PA

PI Mao Y, Xie Y;
 XX WPI; 2003-222563/22.
 DR N-PSDB; ACC00158.
 XX Polypeptide-kinesin-38.28 and polynucleotide for coding this polypeptide.
 PT Claim 1; Page 28-29; 32pp; Chinese.
 XX The present invention discloses a polypeptide-kinesin-38.28, The
 CC invention also discloses the method for curing several diseases, such as
 CC paralytic, arrhythmia, bronchial asthma, peptic ulcer and dementia by
 CC using the polypeptide. The present sequence represents kinesin 38.28
 XX Sequence 348 AA;
 SQ Query Match 65.8%; Score 52; DB 6; Length 348;
 Best Local Similarity 66.7%; Pred. No. 1.2;
 Matches 10; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
 QY 1 RHYGETKMNQSRSS 15
 DB 11 RHTGTTQMNEHSRS 25
 RESULT 23
 ABR80078
 ID ABR80078 standard; protein; 1279 AA.
 XX ABR80078;
 AC 27-AUG-2002 (first entry)
 DT Human kinesin motor protein (HsKrp5) amino acid sequence.
 DE Human; kinesin motor protein; HsKrp5; cytostatic; cardiovascular;
 KW immunomodulatory; anti-inflammatory; vaccine; gene therapy;
 KW spindle morphogenesis; chromosome; cell division;
 KW cellular proliferation disorder; cancer; hyperplasia; restenosis;
 KW cardiac hypertrophy; immune disorder; inflammation.
 XX Homo sapiens.
 OS Key Location/Qualifiers
 FH Misc-difference 409..446
 FT /label= Xaa
 FT /note= "Xaa may be any amino acid"
 XX US6379941-B1.
 XX 30-APR-2002.
 XX 27-NOV-2000; 2000US-00724517.
 XX 17-AUG-2000; 2000US-00641807.
 XX (CYTO-) CYTOKINETICS INC.
 XX Beraud C, Freedman R;
 PI WPI; 2002-413719/44.
 XX N-PSDB; ABL58668.
 XX Isolated human kinesin motor protein HsKrp5, useful for preventing,
 PT diagnosing and treating e.g. cancer, hyperplasias, restenosis, cardiac
 PT hypertrophy, immune disorders and inflammation.
 XX Claim 4; Fig 2; 29pp; English.
 PS The invention relates to an isolated human kinesin motor protein
 CC (HsKrp5). The activity of the protein may be described
 CC as cytostatic, cardiovascular, immunomodulatory and anti-inflammatory.
 CC The protein may be used in a vaccine or in gene therapy. Kinesin-related

CC proteins (KRP5) participate in spindle morphogenesis and chromosome
 CC movement in cell division. The anti-Hskrp5 agonists, antibodies and
 CC anti-Hskrp5 antibodies may also be used as diagnostic agents for
 CC detecting the presence of Hskrp5 in samples (e.g. by enzyme linked
 CC immunosorbant assay (ELISA)) and therefore diagnose diseases associated
 CC with aberrant Hskrp5 expression and activity. They may be used in this
 CC way to prevent, diagnose and treat cellular proliferation disorders e.g.
 CC cancer, hyperplasias, restenosis, cardiac hypertrophy, immune disorders
 CC and inflammation. The current sequence represents the human kinesin motor
 CC protein (Hskrp5) amino acid sequence
 XX
 SQ Sequence 1279 AA;

Query Match 65.8%; Score 52; DB 5; Length 1279;
 Best Local Similarity 66.7%; Pred. No. 4.9;
 Matches 10; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 RHVGETKNQSRSS 15
 |||:|:|:|
 Db 194 RHTGTTQMHSSRS 208

RESULT 24
 ABG70787
 ID ABG70787 standard; protein; 1279 AA.
 XX
 AC ABG70787;
 XX
 DT 12-DEC-2002 (first entry)
 XX
 DE Human kinesin-related protein 5 (Hskrp5) protein.
 XX
 KW Human; kinesin-related protein 5; Hskrp5; motor protein; microtubule;
 KW ATPase activity; Krp; spindle morphogenesis; chromosome movement;
 KW cell division; diagnostic; therapeutic; biopsied tissue; cancer; tumour;
 KW psoriasis; keloid; neurological disorder; autoimmune disease; arthritis;
 KW graft rejection; inflammatory bowel disease; vesicular transport;
 KW antiinflammatory.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT Domain 3..343
 FT /label= Motor domain
 FT /note= "This domain is specifically claimed in claim 3"
 FT Misc-difference 409..446
 FT /label= Unknown
 FT /note= "Residues are not defined in the specification"
 XX
 PN US6440731-B1.
 XX
 PD 27-AUG-2002.
 XX
 PF 17-AUG-2000; 2000US-00641807.
 XX
 PR 17-AUG-2000; 2000US-00641807.
 XX
 PA (CYTO-) CYTOKINETICS INC.
 XX
 PI Beraud C, Freedman R;
 XX
 DR WPI; 2002-739590/80.
 DR N-PSDB; ABS54500.
 XX
 XX Novel isolated nucleic acid sequence encoding a motor protein, useful for
 PT diagnosing, preventing and treating cancer, psoriasis, keloids,
 PT neurological disorders and disorders of vesicular transport.
 XX
 PS Claim 3; Fig 2; 30pp; English.
 XX
 CC The invention discloses an isolated nucleic acid which encodes a human
 CC kinesin-related motor protein (Hskrp5) that has a microtubule stimulated

CC ATPase activity. Krps participate in spindle morphogenesis and chromosome
 CC movement in cell division. The Hskrp5 nucleic acid is useful for
 CC diagnostic purposes to determine the presence, or absence, and excess
 CC expression of Hskrp5 and to monitor the regulation of Hskrp5 levels
 CC during therapeutic intervention. The nucleic acid is also useful to
 CC detect and quantitate gene expression in biopsied tissues in which Hskrp5
 CC may be correlated with the disease and in assays to detect the presence
 CC of associated disorders. The nucleic acid and its encoded protein are
 CC useful in diagnosing, preventing and treating cancer, tumours, psoriasis,
 CC keloids, neurological disorders, autoimmune disease, arthritis, graft
 CC rejection, inflammatory bowel disease and disorders of vesicular
 CC transport. The sequence presented is the human Hskrp5 protein
 XX
 SQ Sequence 1279 AA;

Query Match 65.8%; Score 52; DB 5; Length 1279;
 Best Local Similarity 66.7%; Pred. No. 4.9;
 Matches 10; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 RHVGETKNQSRSS 15
 |||:|:|:|
 Db 194 RHTGTTQMHSSRS 208

RESULT 25
 ABG72397
 ID ABG72397 standard; protein; 1279 AA.
 XX
 AC ABG72397;
 XX
 DT 11-FEB-2003 (first entry)
 XX
 DE Human partial kinesin protein, Hskrp5.
 XX
 KW Human; kinesin; Hskrp5; ATPase; microtubule; cellular proliferation;
 KW cancer; hyperplasia; restenosis; cardiac hypertrophy; autoimmune disease;
 KW immune disorder; arthritis; graft rejection; inflammatory bowel disease;
 KW inflammation; neurological disorder; vesicular transport disorder;
 KW enzyme.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT Misc-difference 409
 FT /label= UNKNOWN
 FT /note= "Encoded by TNN"
 FT Misc-difference 410..445
 FT /label= UNKNOWN
 FT /note= "Encoded by nucleotides 1336-1339 of the DNA
 FT sequence appearing as ABX13613"
 FT Misc-difference 446
 FT /label= UNKNOWN
 FT /note= "Encoded by NGA"
 XX
 PN US6448026-B1.
 XX
 PD 10-SEP-2002.
 XX
 PF 27-NOV-2000; 2000US-00723096.
 XX
 PR 17-AUG-2000; 2000US-00641807.
 XX
 PA (CYTO-) CYTOKINETICS INC.
 XX
 PI Beraud C, Freedman R;
 XX
 DR WPI; 2003-089119/08.
 DR N-PSDB; ABX13613.
 XX
 XX Screening for modulators of human kinesin protein Hskrp5, which are
 PT useful in treating cancers or restenosis, comprises detecting binding or
 PT ATPase activity levels of the protein in a first and second concentration
 PT of a candidate agent.

XX Claim 5; Fig 2; 30pp; English.

XX The invention relates to screening for modulators of a target protein,

CC comprises detecting the level of binding activity or ATPase activity of

CC the target protein when contacted with a first and second concentration

CC of a candidate agent. The target protein comprises a sequence that has

CC greater than 90% amino acid identity with a sequence of human kinesin

CC protein HsKrp5 (or its motor domain). The method is useful for screening

CC for modulators of a target protein having microtubule stimulated ATPase

CC activity, particularly the human kinesin protein HsKrp5. The modulators

CC of HsKrp5 are useful in diagnosing, preventing or treating cellular

CC proliferation (e.g. cancers (many examples given in the specification) or

CC hyperplasia), restenosis, cardiac hypertrophy, autoimmune disease, immune

CC disorders, arthritis, graft rejection, inflammatory bowel disease,

CC inflammation, neurological disorders, or disorders of vesicular

CC transport. The present sequence represents human HsKrp5

XX

XX Sequence 1279 AA;

Query Match 65.8%; Score 52; DB 6; Length 1279;

Best Local Similarity 66.7%; Pred. No. 4.9;

Matches 10; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 RHYGETQMQRSSRS 15

DB 194 RHTGTTQMNESSRS 208

|||||:||||

RESULT 26

ADJ94914

ID ADJ94914 standard; protein; 1401 AA.

XX

XX ADJ94914;

XX

DT 06-MAY-2004 (first entry)

XX

DE Novel NOVX protein sequence #71.

XX

XX antidiabetic; anorectic; cardiast; hypotensive; antiarteriosclerotic;

XX anorectic; virucide; antibacterial; fungicide; protozoicide; nootropic;

KW neuroprotective; antiparkinsonian; anticonvulsant; osteopathic;

KW antirheumatic; antiinflammatory; dermatological; antiasthmatic;

KW antilipemic; gene therapy; metabolic disorder; diabetes; obesity;

KW infectious disease; anorexia; cancer; cardiovascular disease;

KW hypertension; atherosclerosis; neurodegenerative disorder; immune disorder;

KW Alzheimer's disease; Parkinson's disease; epilepsy; inflammatory skin disorder;

KW osteoarthritis; hematopoietic disorder; cell differentiation;

KW asthma; dyslipidemia; neurogenesis; wound healing; angiogenesis;

KW cell proliferation; hematopoiesis; tissue typing; pharmacogenomic.

KW

XX

OS Homo sapiens.

XX

XX WO2003040325-A2.

PN

XX

PD 15-MAY-2003.

XX

XX

PF 05-NOV-2002; 2002WO-US035464.

XX

XX 05-NOV-2001; 2001US-0338626P.

PR

PR 06-NOV-2001; 2001US-0333072P.

PR

PR 09-NOV-2001; 2001US-0348283P.

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PR 15-NOV-2001; 2001US-0335610P.

PR

PR 16-NOV-2001; 2001US-0338543P.

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PR 20-NOV-2001; 2001US-0331630P.

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PR 21-NOV-2001; 2001US-0331641P.

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PR 27-NOV-2001; 2001US-0332152P.

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PR 28-NOV-2001; 2001US-0333461P.

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PR 30-NOV-2001; 2001US-0334300P.

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30-NOV-2001; 2001US-0334526P.

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04-DEC-2001; 2001US-0336576P.

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04-DEC-2001; 2001US-033664P.

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07-DEC-2001; 2001US-0338314P.

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10-DEC-2001; 2001US-0338390P.

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10-DEC-2001; 2001US-0339006P.

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01-FEB-2002; 2002US-033280P.

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01-FEB-2002; 2002US-0353280P.

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04-FEB-2002; 2002US-0354392P.

PR

04-FEB-2002; 2002US-0354393P.

PR

04-FEB-2002; 2002US-0354409P.

PR

27-FEB-2002; 2002US-035944P.

PR

27-FEB-2002; 2002US-0360148P.

PR

05-MAR-2002; 2002US-0361790P.

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05-MAR-2002; 2002US-0361833P.

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13-MAR-2002; 2002US-0364000P.

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13-MAR-2002; 2002US-0364182P.

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28-MAY-2002; 2002US-0381621P.

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06-AUG-2002; 2002US-0401552P.

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PR

23-AUG-2002; 2002US-0405402P.

PR

23-AUG-2002; 2002US-0405496P.

PR

23-AUG-2002; 2002US-0405631P.

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26-AUG-2002; 2002US-0406125P.

PR

04-NOV-2002; 2002US-00287226.

XX

(CURA-) CURAGEN CORP.

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Chaudhuri A, Dipippo VA, Edinger SR, Eisele A, Ellerman K;

Gangolli EA, Gorman L, Gerlach VL, Ji W, Kekuda R, Khramtsov NV;

Li L, Malyankar UM, MacDougall JR, Mezes PS, Miller CE, Millet I;

Ooi CE, Ort T, Padigaru M, Patturajan M, Rastelli L, Rieger DK;

Rothenberg ME, Shenoy SG, Spaderna SK, Spytek KA, Taupier RJ;

Vernet CAM, Zerhusen BD, Zhong M;

WPI; 2003-441551/41.

N-PSDB; ADJ94913.

XX

XX New isolated NOVX polypeptides and polynucleotides, useful for

PT preventing, diagnosing or treating NOVX-associated disorders, e.g.

PT osteoarthritis, obesity, atherosclerosis, cancer, Parkinson's disease,

PT asthma, or infections.

XX

XX Claim 1; SEQ ID NO 142; 800pp; English.

XX

XX The invention relates to novel isolated polypeptides, mature forms of

CC these, or a sequence that is at least 95 % identical to, or having one or

CC more conservative amino acid substitutions in the polypeptides. The

CC polypeptides, nucleic acid molecules and antibodies are useful in the

CC manufacture of a medicament for treating a syndrome associated with a

CC human disease, preferably a NOVX-associated disorder. The nucleic acid

CC molecules, polypeptides and antibodies are useful for treating

CC preventing or diagnosing diseases such as metabolic disorders, diabetes, and

CC obesity, infectious diseases (viral, bacterial, fungal, helminthic, and

CC protozoal), anorexia, cancer, cardiovascular diseases (hypertension,

CC atherosclerosis), neurodegenerative disorders (Alzheimer's disease,

CC Parkinson's disease, epilepsy, immune disorders (osteoarthritis),

CC hematopoietic disorders, inflammatory skin disorders, asthma, and various

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PR 18-JUN-1999;	99US-0139461P.	PR 23-AUG-1999;	99US-0149930P.
PR 18-JUN-1999;	99US-0139462P.	PR 25-AUG-1999;	99US-0150566P.
PR 18-JUN-1999;	99US-0139463P.	PR 26-AUG-1999;	99US-0150884P.
PR 18-JUN-1999;	99US-0139750P.	PR 27-AUG-1999;	99US-0151065P.
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PR 21-JUN-1999;	99US-0139811P.	PR 27-AUG-1999;	99US-0151080P.
PR 22-JUN-1999;	99US-0139899P.	PR 30-AUG-1999;	99US-0151303P.
PR 23-JUN-1999;	99US-0140353P.	PR 31-AUG-1999;	99US-0151438P.
PR 23-JUN-1999;	99US-0140354P.	PR 07-SEP-1999;	99US-0151930P.
PR 23-JUN-1999;	99US-0140695P.	PR 10-SEP-1999;	99US-0152363P.
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PR 28-JUN-1999;	99US-0140991P.	PR 13-SEP-1999;	99US-0153758P.
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PR 01-JUL-1999;	99US-0141842P.	PR 16-SEP-1999;	99US-0154039P.
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PR 02-JUL-1999;	99US-0142055P.	PR 22-SEP-1999;	99US-0155139P.
PR 06-JUL-1999;	99US-0142390P.	PR 23-SEP-1999;	99US-0155486P.
PR 08-JUL-1999;	99US-0142803P.	PR 24-SEP-1999;	99US-0155659P.
PR 09-JUL-1999;	99US-0142920P.	PR 28-SEP-1999;	99US-0156458P.
PR 12-JUL-1999;	99US-0142977P.	PR 29-SEP-1999;	99US-0156596P.
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PR 14-JUL-1999;	99US-0143624P.	PR 05-OCT-1999;	99US-0157753P.
PR 15-JUL-1999;	99US-0144005P.	PR 06-OCT-1999;	99US-0157865P.
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PR 16-JUL-1999;	99US-0144325P.	PR 08-OCT-1999;	99US-0158232P.
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PR 21-JUL-1999;	99US-0144884P.	PR 18-OCT-1999;	99US-0159638P.
PR 21-JUL-1999;	99US-0144814P.	PR 21-OCT-1999;	99US-0159584P.
PR 21-JUL-1999;	99US-0145086P.	PR 21-OCT-1999;	99US-0160741P.
PR 21-JUL-1999;	99US-0145088P.	PR 21-OCT-1999;	99US-0160767P.
PR 22-JUL-1999;	99US-0145087P.	PR 21-OCT-1999;	99US-0160768P.
PR 22-JUL-1999;	99US-0145089P.	PR 21-OCT-1999;	99US-0160770P.
PR 22-JUL-1999;	99US-0145192P.	PR 21-OCT-1999;	99US-0160814P.
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PR 23-JUL-1999;	99US-0145218P.	PR 22-OCT-1999;	99US-0160980P.
PR 23-JUL-1999;	99US-0145224P.	PR 22-OCT-1999;	99US-0160981P.
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PR 27-JUL-1999;	99US-0145913P.	PR 25-OCT-1999;	99US-0161404P.
PR 27-JUL-1999;	99US-0145918P.	PR 25-OCT-1999;	99US-0161405P.
PR 27-JUL-1999;	99US-0145919P.	PR 25-OCT-1999;	99US-0161406P.
PR 28-JUL-1999;	99US-0145911P.	PR 26-OCT-1999;	99US-0161359P.
PR 02-AUG-1999;	99US-0146386P.	PR 26-OCT-1999;	99US-0161360P.
PR 02-AUG-1999;	99US-0146388P.	PR 26-OCT-1999;	99US-0161361P.
PR 02-AUG-1999;	99US-0146389P.	PR 28-OCT-1999;	99US-0161920P.
PR 03-AUG-1999;	99US-0147038P.	PR 28-OCT-1999;	99US-0161992P.
PR 04-AUG-1999;	99US-0147204P.	PR 28-OCT-1999;	99US-0161993P.
PR 04-AUG-1999;	99US-0147302P.	PR 29-OCT-1999;	99US-0162142P.
PR 05-AUG-1999;	99US-0147192P.		
PR 05-AUG-1999;	99US-0147260P.		
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PR 09-AUG-1999;	99US-0147493P.		
PR 09-AUG-1999;	99US-0147993P.		
PR 10-AUG-1999;	99US-0148171P.		
PR 11-AUG-1999;	99US-0148319P.		
PR 12-AUG-1999;	99US-0148341P.		

Query Match 64.6%; Score 51; DB 3; Length 726;
Best Local Similarity 66.7%; Pred. No. 4;
Matches 10; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 1 RHYGETKNORSRS 15
Db 106 RKIGETSLNRSRS 120

PR	20-AUG-1999;	99US-0149929P.	XX	Arabidopsis thaliana protein fragment SEQ ID NO: 37315.
PR	23-AUG-1999;	99US-0149902P.	DE	
PR	23-AUG-1999;	99US-0149930P.	XX	Protein identification; signal transduction pathway; metabolic pathway;
PR	25-AUG-1999;	99US-0150566P.	KW	hybridisation assay; genetic mapping; gene expression control; promoter;
PR	26-AUG-1999;	99US-0150884P.	KW	termination sequence.
PR	27-AUG-1999;	99US-0151065P.	XX	
PR	27-AUG-1999;	99US-0151068P.	OS	Arabidopsis thaliana.
PR	27-AUG-1999;	99US-0151080P.	XX	
PR	30-AUG-1999;	99US-0151303P.	PN	EP1033405-A2.
PR	31-AUG-1999;	99US-0151438P.	XX	
PR	01-SEP-1999;	99US-0151930P.	XX	
PR	07-SEP-1999;	99US-0152363P.	PD	06-SEP-2000.
PR	10-SEP-1999;	99US-0153070P.	XX	
PR	13-SEP-1999;	99US-0153758P.	PF	25-FEB-2000; 2000EP-00301439.
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RESULT 31
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KW Drosophila; developmental biology; cell signalling; insecticide;
pharmaceutical.
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OS Drosophila melanogaster.

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XX WO200171042-A2.
XX 27-SEP-2001.
XX 23-MAR-2001; 2001WO-US009231.
XX 23-MAR-2000; 2000US-0191637P.
XX 11-JUL-2000; 2000US-00614150.
XX (PEKE ) PE CORP NV.
XX Venter JC, Adams M, Li PWD, Myers EW;
XX WPI; 2001-656860/75.
XX N-PSDB; ABL09286.
XX New isolated nucleic acid detection reagent for detecting 1000 or more
XX genes from Drosophila and for elucidating cell signaling and cell-cell
XX interactions.
XX Disclosure; SEQ ID NO 22341; 21pp + Sequence Listing; English.
XX The invention relates to an isolated nucleic acid detection reagent
XX capable of detecting 1000 or more genes from Drosophila. The invention is
XX useful in developmental biology and in elucidating cell signalling and
XX cell-cell interactions in higher eukaryotes for the development of
XX insecticides, therapeutics and pharmaceutical drugs. The invention
XX discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA
XX sequences (ABL01840-ABL16175) and the encoded proteins (ABB57737-
XX ABB72072). The sequence data for this patent did not form part of the
XX printed specification, but was obtained in electronic format directly
XX from WIPO at fcp.wipo.int/pub/published_pct_sequences
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XX KW Protein identification; signal transduction pathway; metabolic pathway;
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XX OS Arabidopsis thaliana.
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 PR 25-OCT-1999; 99US-0161406P.
 PR 26-OCT-1999; 99US-0161359P.
 PR 26-OCT-1999; 99US-0161360P.
 PR 26-OCT-1999; 99US-0161361P.
 PR 28-OCT-1999; 99US-0161920P.
 PR 28-OCT-1999; 99US-0161922P.
 PR 28-OCT-1999; 99US-0161993P.
 PR 29-OCT-1999; 99US-0162142P.

Query Match 62.0%; Score 49; DB 3; Length 172;
 Best Local Similarity 72.7%; Pred No. 1.9;
 Matches 8; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 RHYGETKMNQR 11
 ||| ||::|||
 Db 68 RHYNETRINQR 78

RESULT 33
 ADC23342

ID ADC23342 standard; protein; 346 AA.

XX AC ADC23342;

XX DT 18-DEC-2003 (first entry)

XX DE Human kinesin-like DNA binding protein (KID) (SeqID 6).

XX KW human; enzyme; motor domain; kinesin-like DNA binding protein; KID;
 KW cytoskeletal; cardiant; immunomodulator; antiinflammatory; gene therapy;
 KW cancer; hyperplasia; restenosis; cellular proliferation disorder;
 KW cardiac hypertrophy; immune disorder; inflammation.

XX OS Homo sapiens.

XX PN US6387644-B1.

XX PD 14-MAY-2002.

XX PF 28-NOV-2000; 2000US-00724224.

XX PR 20-APR-1999; 99US-00395612.

XX PR 20-JUN-2000; 2000US-00597292.

XX PA (CYTO-) CYTOKINETICS INC.

XX PI Beraud C;

XX WPI; 2003-706919/67.

DR N-PSDB; ADC23341.

PT Identifying a candidate agent as modulator of function of a target
 protein for treating cellular proliferation disorders by adding a

CC for modulators of a motor protein which has microtubule stimulated ATPase
 CC activity, a method of testing for ATPase activity of microtubule motor
 CC proteins, methods to identify candidate agents that bind to a target
 CC protein or act as a modulator of the binding characteristics or
 CC biological activity of a target protein, modulators of the target
 CC protein, and methods of treating cellular proliferation disorders such as
 CC cancer, hyperplasias, restenosis, cardiac hypertrophy, immune disorders
 CC and inflammation, for treating disorders associated with kinesin-like DNA
 CC binding protein (KID) and for inhibiting KID. The sequences are used for
 CC screening for modulators of motor proteins useful for treating cellular
 CC proliferation disorders such as cancer, hyperplasias, restenosis, cardiac
 CC hypertrophy, immune disorders and inflammation, for treating disorders
 CC associated with KID and for inhibiting KID and for treating autoimmune
 CC diseases, arthritis, graft rejection, inflammatory bowel disease and
 CC proliferation induced after medical procedures including surgery and
 CC angioplasty. This sequence represents a human microtubule motor protein
 CC of the invention.
 XX
 SQ Sequence 346 AA;
 Query Match 62.0%; Score 49; DB 8; Length 346;
 Best Local Similarity 66.7%; Pred. No. 4;
 Matches 10; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
 Qy 1 RHYGETKMQRSRS 15
 Db 208 RTVGATRLNQRSRS 222
 RESULT 35
 ADQ88357
 ID ADQ88357 standard; protein; 346 AA.
 XX
 AC ADQ88357;
 XX
 DT 07-OCT-2004 (first entry)
 XX
 DE Human microtubule motor protein KID #3.
 XX
 KW Human; microtubule motor protein; cellular proliferative disorder;
 KW cancer; hyperplasia; restenosis; cardiac hypertrophy; immune disorder;
 KW wound; inflammation; autoimmune disease; arthritis;
 KW inflammatory bowel disease; solid tumour; skin carcinoma;
 KW breast carcinoma; cervical carcinoma; testicular carcinoma;
 KW bronchogenic carcinoma; alveolar carcinoma; adenocarcinoma; bone tumour;
 KW osteogenic sarcoma; multiple myeloma; malignant melanoma; KID.
 XX
 OS Homo sapiens.
 XX
 PN US2004142397-A1.
 XX
 PD 22-JUL-2004.
 XX
 PF 09-MAR-2004; 2004US-00797893.
 XX
 PR 20-APR-1999; 99US-00295612.
 PR 20-JUN-2000; 2000US-00597292.
 PR 28-NOV-2000; 2000US-00724224.
 PR 06-MAR-2002; 2002US-00093317.
 XX
 PA (CYTO-) CYTOKINETICS INC.
 XX
 PI Beraud C;
 XX
 DR WPI; 2004-552562/53.
 DR N-PSDB; ADQ88356.
 XX
 PT Novel isolated microtubule motor protein, useful for identifying
 PT candidate agent modulating function of protein, for treating cellular
 PT proliferative diseases such as cancer, restenosis, cardiac hypertrophy
 PT and inflammation.
 XX
 PS Claim 5; SEQ ID NO 6; 27pp; English.

PT candidate agent to a mixture of the target protein that
 PT directly/indirectly produces ADP or phosphate.
 XX
 PS Claim 1; SEQ ID NO 6; 26pp; English.
 XX
 CC This invention relates to a novel method for high throughput screening
 CC systems used to identify compounds for the treatment of cellular
 CC proliferation disorders. Specifically, it refers to candidate agents that
 CC are capable of modulating the activity of target proteins having motor
 CC domains, such that the target protein directly or indirectly produces ADP
 CC or phosphate. Furthermore, this activity can be determined using
 CC fluorescence or absorbance readouts. The present invention describes a
 CC method that identifies modulators of the target protein, which is a
 CC kinesin-like DNA binding protein (known as KID) as cytosolic, cardants,
 CC immunomodulators and antiinflammatory. Accordingly, through gene
 CC therapy, they can be used for the treatment of cancer, hyperplasias,
 CC restenosis, cardiac hypertrophy, immune disorders and inflammation. This
 CC polypeptide sequence is human KID protein (SeqID 6) of the invention.
 XX
 SQ Sequence 346 AA;
 Query Match 62.0%; Score 49; DB 7; Length 346;
 Best Local Similarity 66.7%; Pred. No. 4;
 Matches 10; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
 Qy 1 RHYGETKMQRSRS 15
 Db 208 RTVGATRLNQRSRS 222
 RESULT 34
 ADQ60232
 ID ADQ60232 standard; protein; 346 AA.
 XX
 AC ADQ60232;
 XX
 DT 23-SEP-2004 (first entry)
 XX
 DE Human microtubule motor protein #3.
 XX
 KW Human; microtubule motor protein; cellular proliferation disorder;
 KW cancer; hyperplasia; restenosis; cardiac hypertrophy; immune disorder;
 KW inflammation; kinesin-like DNA binding protein; KID; autoimmune disease;
 KW arthritis; graft rejection; inflammatory bowel disease; angioplasty.
 XX
 OS Homo sapiens.
 XX
 PN US6762043-B1.
 XX
 PD 13-JUL-2004.
 XX
 PF 06-MAR-2002; 2002US-00093317.
 XX
 PR 20-APR-1999; 99US-00295612.
 PR 20-JUN-2000; 2000US-00597292.
 PR 28-NOV-2000; 2000US-00724224.
 XX
 PA (CYTO-) CYTOKINETICS INC.
 XX
 PI Beraud C;
 XX
 DR WPI; 2004-532491/51.
 DR N-PSDB; ADQ60231.
 XX
 PT New isolated microtubule motor protein, useful for screening modulators
 PT for treating cellular proliferation disorders such as cancer,
 PT hyperplasias, restenosis, cardiac hypertrophy, immune disorders and
 PT inflammation.
 XX
 PS Claim 1; SEQ ID NO 6; 26pp; English.
 XX
 CC The invention relates to human microtubule motor proteins and the nucleic
 CC acids encoding them. The invention also relates to a method of screening

XX The invention relates to microtubule motor proteins and nucleic acid
 CC molecules encoding such proteins. Microtubule motor proteins are useful
 CC for identifying candidate agents modulating the function of protein which
 CC in turn are useful for treating cellular proliferative disorders such as
 CC cancer, hyperplasia, restenosis, cardiac hypertrophy, immune disorders,
 CC wounds and inflammation. Other disorders treated include autoimmune
 CC disease, arthritis, inflammatory bowel disease, solid tumours such as
 CC skin carcinomas, breast carcinomas, cervical carcinomas, testicular
 CC carcinomas, bronchogenic carcinoma, alveolar carcinoma, adenocarcinoma,
 CC tumour of bone such as osteogenic sarcoma, multiple myeloma, malignant
 CC melanoma etc. The present sequence is a human microtubule motor protein
 CC KID polypeptide.

XX Sequence 346 AA;
 SQ

Query Match 62.0%; Score 49; DB 8; Length 346;
 Best Local Similarity 66.7%; Pred. No. 4;
 Matches 10; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 RHYGETKNQSRSS 15
 | | | | | | | | | |
 Db 208 RTVGATRLNQSRSS 222

RESULT 36
 ADC23338
 ID ADC23338 standard; protein; 370 AA.
 AC ADC23338;
 XX
 DT 18-DEC-2003 (first entry)
 XX
 DE Human kinesin-like DNA binding protein (KID) (SeqID 2).
 XX
 KW human; enzyme; motor domain; kinesin-like DNA binding protein; KID;
 KW cytosolic; cardiac; immunomodulator; antiinflammatory; gene therapy;
 KW cancer; hyperplasia; restenosis; cellular proliferation disorder;
 KW cardiac hypertrophy; immune disorder; inflammation.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT Misc-difference 1 /note= "Encoded by ATGCA"
 XX
 PN US6387644-B1.
 XX
 PD 14-MAY-2002.
 XX
 PF 28-NOV-2000; 2000US-00724224.
 XX
 PR 20-APR-1999; 99US-00295612.
 PR 20-JUN-2000; 2000US-00597292.
 XX
 PA (CYTO-) CYTOKINETICS INC.
 XX
 PI Beraud C;
 XX
 DR WPI: 2003-706919/67.
 DR N-PSDB; ADC23337.
 XX
 XX Identifying a candidate agent as modulator of function of a target
 PT protein for treating cellular proliferation disorders by adding a
 PT candidate agent to a mixture of the target protein that
 PT directly/indirectly produces ADP or phosphate.
 XX
 PS Claim 1; SEQ ID NO 2; 26pp; English.
 XX
 XX This invention relates to a novel method for high throughput screening
 CC systems used to identify compounds for the treatment of cellular
 CC proliferation disorders. Specifically, it refers to candidate agents that
 CC are capable of modulating the activity of target proteins having motor

CC domains, such that the target protein directly or indirectly produces ADP
 CC or phosphate. Furthermore, this activity can be determined using
 CC fluorescence or absorbance readouts. The present invention describes a
 CC method that identifies modulators of the target protein, which is a
 CC kinesin-like DNA binding protein (known as KID) as cytosolic, cardiac,
 CC immunomodulators and antiinflammatory. Accordingly, through gene
 CC therapy, they can be used for the treatment of cancer, hyperplasias,
 CC restenosis, cardiac hypertrophy, immune disorders and inflammation. This
 CC polypeptide sequence is human KID protein (SeqID 2) of the invention.

XX Sequence 370 AA;
 SQ

Query Match 62.0%; Score 49; DB 7; Length 370;
 Best Local Similarity 66.7%; Pred. No. 4.3;
 Matches 10; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 RHYGETKNQSRSS 15
 | | | | | | | | | |
 Db 232 RTVGATRLNQSRSS 246

RESULT 37
 ADQ60228
 ID ADQ60228 standard; protein; 370 AA.
 XX
 AC ADQ60228;
 XX
 DT 23-SEP-2004 (first entry)
 XX
 DE Human microtubule motor protein #1.
 XX
 KW Human; microtubule motor protein; cellular proliferation disorder;
 KW cancer; hyperplasia; restenosis; cardiac hypertrophy; immune disorder;
 KW inflammation; kinesin-like DNA binding protein; KID; autoimmune disease;
 KW arthritis; graft rejection; inflammatory bowel disease; angioplasty.
 XX
 OS Homo sapiens.
 XX
 PN US6762043-B1.
 XX
 PD 13-JUL-2004.
 XX
 PF 06-MAR-2002; 2002US-00093317.
 XX
 PR 20-APR-1999; 99US-00295612.
 PR 20-JUN-2000; 2000US-00597292.
 PR 28-NOV-2000; 2000US-00724224.
 XX
 PA (CYTO-) CYTOKINETICS INC.
 XX
 PI Beraud C;
 XX
 DR WPI: 2004-532491/51.
 XX
 PT New isolated microtubule motor protein, useful for screening modulators
 PT for treating cellular proliferation disorders such as cancer,
 PT hyperplasias, restenosis, cardiac hypertrophy, immune disorders and
 PT inflammation.
 XX
 PS Claim 1; SEQ ID NO 2; 26pp; English.
 XX
 XX The invention relates to human microtubule motor proteins and the nucleic
 CC acids encoding them. The invention also relates to a method of screening
 CC for modulators of a motor protein which has microtubule stimulated ATPase
 CC activity, a method of testing for ATPase activity of microtubule motor
 CC proteins, methods to identify candidate agents that bind to a target
 CC protein or act as a modulator of the binding characteristics or
 CC biological activity of a target protein, modulators of the target
 CC protein, and methods of treating cellular proliferation disorders such as
 CC cancer, hyperplasias, restenosis, cardiac hypertrophy, immune disorders
 CC and inflammation, for treating disorders associated with kinesin-like DNA
 CC binding protein (KID) and for inhibiting KID. The sequences are used for
 CC screening for modulators of motor proteins useful for treating cellular

CC proliferation disorders such as cancer, hyperplasias, restenosis, cardiac
CC hypertrophy, immune disorders and inflammation, for treating disorders
CC associated with KID and for inhibiting KID and for treating autoimmune
CC diseases, arthritis, graft rejection, inflammatory bowel disease and
CC proliferation induced after medical procedures including surgery and
CC angioplasty. This sequence represents a human microtubule motor protein
CC of the invention. Note: The specification states that this sequence is
CC encoded by the nucleic acid featured as SEQ ID NO:1, but this does not
CC appear to be the case.
XX
XX
SQ Sequence 370 AA;
Query Match 62.0%; Score 49; DB 8; Length 370;
Best Local Similarity 66.7%; Pred. No. 4.3;
Matches 10; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
QY 1 RHYGETKMNQSRSS 15
DB 232 RTVGATRLNQSRSS 246
RESULT 38
ADQ88353
ID ADQ88353 standard; protein; 370 AA.
XX
AC ADQ88353;
XX
XX 07-OCT-2004 (first entry)
XX
XX Human microtubule motor protein KID #1.
XX
XX Human; microtubule motor protein; cellular proliferative disorder;
KW cancer; hyperplasia; restenosis; cardiac hypertrophy; immune disorder;
KW wound; inflammation; autoimmune disease; arthritis;
KW inflammatory bowel disease; solid tumour; skin carcinoma;
KW breast carcinoma; cervical carcinoma; testicular carcinoma;
KW bronchogenic carcinoma; alveolar carcinoma; adenocarcinoma; bone tumour;
KW osteogenic sarcoma; multiple myeloma; malignant melanoma; KID.
XX
XX Homo sapiens.
XX
XX Key Location/Qualifiers
FH Misc-difference 1 /note= "Encoded by ATGCA"
FT
FT
XX US2004142397-A1.
XX
XX 22-JUL-2004.
XX
XX 09-MAR-2004; 2004US-00797893.
XX
XX 20-APR-1999; 99US-00295612.
XX 20-JUN-2000; 2000US-00597292.
XX 28-NOV-2000; 2000US-00724224.
XX 06-MAR-2002; 2002US-00093317.
XX (CYTO-) CYTOKINETICS INC.
XX
XX Beraud C;
XX
XX WPI; 2004-552562/53.
XX N-PSDB; ADQ88352.
XX Novel isolated microtubule motor protein, useful for identifying
FT candidate agent modulating function of protein, for treating cellular
FT proliferative diseases such as cancer, restenosis, cardiac hypertrophy
FT and inflammation.
XX
XX Claim 5; SEQ ID NO 2; 27pp; English.
XX
XX The invention relates to microtubule motor proteins and nucleic acid
CC molecules encoding such proteins. Microtubule motor proteins are useful
CC for identifying candidate agents modulating the function of protein which

CC in turn are useful for treating cellular proliferative disorders such as
CC cancer, hyperplasia, restenosis, cardiac hypertrophy, immune disorders,
CC wounds and inflammation. Other disorders treated include autoimmune
CC disease, arthritis, inflammatory bowel disease, solid tumours such as
CC skin carcinomas, breast carcinomas, cervical carcinomas, testicular
CC carcinomas, bronchogenic carcinoma, alveolar carcinoma, adenocarcinoma,
CC tumour of bone such as osteogenic sarcoma, multiple myeloma, malignant
CC melanoma etc. The present sequence is a human microtubule motor protein
CC KID polypeptide.
XX
XX SQ Sequence 370 AA;
Query Match 62.0%; Score 49; DB 8; Length 370;
Best Local Similarity 66.7%; Pred. No. 4.3;
Matches 10; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
QY 1 RHYGETKMNQSRSS 15
DB 232 RTVGATRLNQSRSS 246
RESULT 39
AAB56650
ID AAB56650 standard; protein; 460 AA.
XX
AC AAB56650;
XX
XX 13-MAR-2001 (first entry)
XX
XX Human prostate cancer antigen protein sequence SEQ ID NO:1228.
XX
XX Human; prostate cancer; prostate cancer antigen; detection; diagnosis;
KW neuroprotective; cytostatic; cardioprotective; immunomodulatory; muscular;
KW vulvare; gastrointestinal; nephrotropic; antiinfective; gynaecological;
KW antibacterial; gene therapy; neural; immune; reproductive; renal;
KW gastrointestinal; pulmonary; cardiovascular; proliferative disorder;
KW wound; infectious disease.
XX
XX Homo sapiens.
XX
XX WO200055174-A1.
XX
XX 21-SEP-2000.
XX
XX 08-MAR-2000; 2000WO-US005988.
XX
XX 12-MAR-1999; 99US-0124270P.
XX
XX (HUMA-) HUMAN GENOME SCI INC.
XX (ROSE/) ROSEN C A.
XX
XX Rosen CA, Ruben SM;
XX
XX WPI; 2000-587513/55.
XX N-PSDB; AAF15853.
XX
XX Prostate cancer associated gene sequences, referred to as prostate cancer
FT antigens, useful for treatment, prevention, and diagnosis of disorders
FT such as prostate cancer.
XX
XX Claim 11; Page 1649-1651; 2338pp; English.
XX
XX AAF15566 to AAF16505 encode the human prostate cancer associated
CC proteins, called prostate cancer antigens, given in AAB56363 to AAB57302.
CC The prostate cancer antigens can have neuroprotective, cytostatic,
CC cardioprotective, immunomodulatory, muscular, vulvare, gastrointestinal,
CC nephrotropic, antiinfective, gynaecological and antibacterial activities,
CC and can be used in gene therapy. The prostate cancer antigen
CC polynucleotides may be used for detection of prostate cancer, chromosome
CC identification, as chromosome markers, and for numerous other diagnostic
CC or research purposes. The prostate cancer antigens may be used to treat
CC disorders such as neural, immune, muscular, reproductive,
CC gastrointestinal, pulmonary, cardiovascular, renal, and proliferative

CC disorders, wounds, and infectious diseases. AAF16506 to AAF16514 to
CC AAB57303 represent sequences used in the exemplification of the present
CC invention
XX
SQ Sequence 460 AA;

Query Match 62.0%; Score 49; DB 3; Length 460;
Best Local Similarity 66.7%; Pred. No. 5.5;
Matches 10; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
QY 1 RHYGETKMQRSRS 15
| | | | | | | | | |
Db 210 RTVGATRLNQRSRS 224

RESULT 40
ADC23344
ID ADC23344 standard; protein; 487 AA.
AC ADC23344;
XX
DT 18-DEC-2003 (first entry)
XX
DE Human kinesin-like DNA binding protein (KID) (SeqID 8).
XX
KW human; enzyme; motor domain; kinesin-like DNA binding protein; KID;
KW cytoskeletal; cardant; immunomodulator; antiinflammatory; gene therapy;
KW cancer; hyperplasia; restenosis; cellular proliferation disorder;
KW cardiac hypertrophy; immune disorder; inflammation.
XX
OS Homo sapiens.
XX
XX US6387644-B1.
PN
PD 14-MAY-2002.
XX
XX 28-NOV-2000; 2000US-00724224.
XX
XX 20-APR-1999; 99US-00295612.
PR
PR 20-JUN-2000; 2000US-00597292.
XX
XX (CYTO-) CYTOKINETICS INC.
PA
PI Beraud C;
XX
XX WPI; 2003-706919/67.
DR
DR N-PSDB; ADC23343.

PT Identifying a candidate agent as modulator of function of a target
PT protein for treating cellular proliferation disorders by adding a
PT candidate agent to a mixture of the target protein that
PT directly/indirectly produces ADP or phosphate.
XX
PS Claim 1; SEQ ID NO 8; 26pp; English.
XX
CC This invention relates to a novel method for high throughput screening
CC systems used to identify compounds for the treatment of cellular
CC proliferation disorders. Specifically, it refers to candidate agents that
CC are capable of modulating the activity of target proteins having motor
CC domains, such that the target protein directly or indirectly produces ADP
CC or phosphate. Furthermore, this activity can be determined using
CC fluorescence or absorbance readouts. The present invention describes a
CC method that identifies modulators of the target protein, which is a
CC kinesin-like DNA binding protein (known as KID) as cytostatic, cardants,
CC immunomodulators and antiinflammatory. Accordingly, through gene
CC therapy, they can be used for the treatment of cancer, hyperplasias, KID
CC restenosis, cardiac hypertrophy, immune disorders and inflammation. This
CC polypeptide sequence is human KID protein (SeqID 8) of the invention.
XX
SQ Sequence 487 AA;

Query Match 62.0%; Score 49; DB 7; Length 487;
Best Local Similarity 66.7%; Pred. No. 5.9;

Matches 10; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
QY 1 RHYGETKMQRSRS 15
| | | | | | | | | |
Db 208 RTVGATRLNQRSRS 222

RESULT 41
ADQ60234
ID ADQ60234 standard; protein; 487 AA.

XX
AC ADQ60234;
XX
DT 23-SEP-2004 (first entry)
XX
DE Human microtubule motor protein #4.
XX
KW Human; microtubule motor protein; cellular proliferation disorder;
KW cancer; hyperplasia; restenosis; cardiac hypertrophy; immune disorder;
KW inflammation; kinesin-like DNA binding protein; KID; autoimmune disease;
KW arthritis; graft rejection; inflammatory bowel disease; angioplasty.
XX
OS Homo sapiens.
XX
XX US6762043-B1.
PN
PD 13-JUL-2004.
XX
XX 06-MAR-2002; 2002US-00093317.
XX
XX 20-APR-1999; 99US-00295612.
PR
PR 20-JUN-2000; 2000US-00597292.
PR
PR 28-NOV-2000; 2000US-00724224.
XX
XX (CYTO-) CYTOKINETICS INC.
PA
PI Beraud C;
XX
XX WPI; 2004-532491/51.
DR
DR N-PSDB; ADQ60233.

PT New isolated microtubule motor protein, useful for screening modulators
PT for treating cellular proliferation disorders such as cancer,
PT hyperplasias, restenosis, cardiac hypertrophy, immune disorders and
PT inflammation.
XX
PS Claim 1; SEQ ID NO 8; 26pp; English.
XX
CC The invention relates to human microtubule motor proteins and the nucleic
CC acids encoding them. The invention also relates to a method of screening
CC for modulators of a motor protein which has microtubule stimulated ATPase
CC activity, a method of testing for ATPase activity of microtubule motor
CC proteins, methods to identify candidate agents that bind to a target
CC protein or act as a modulator of the binding characteristics or
CC biological activity of a target protein, modulators of the target
CC protein, and methods of treating cellular proliferation disorders such as
CC cancer, hyperplasias, restenosis, cardiac hypertrophy, immune disorders
CC and inflammation, for treating disorders associated with kinesin-like DNA
CC binding protein (KID) and for inhibiting KID. The sequences are used for
CC screening for modulators of motor proteins useful for treating cellular
CC proliferation disorders such as cancer, hyperplasias, restenosis, cardiac
CC hypertrophy, immune disorders and inflammation, for treating disorders
CC associated with KID and for inhibiting KID and for treating autoimmune
CC diseases, arthritis, graft rejection, inflammatory bowel disease and
CC proliferation induced after medical procedures including surgery and
CC angioplasty. This sequence represents a human microtubule motor protein
CC of the invention.
XX
SQ Sequence 487 AA;

Query Match 62.0%; Score 49; DB 8; Length 487;
Best Local Similarity 66.7%; Pred. No. 5.9;
Matches 10; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

RESULT 43	
ADK40973	
ID	ADK40973 standard; protein; 490 AA.
XX	
XX	ADK40973;
XX	
AC	06-MAY-2004 (first entry)
XX	
DT	Novel human kinase protein #80.
XX	
XX	cytostatic; immunomodulator; cardiant; neuroprotective; nootropic;
XX	antiparkinsonian; virucide; antibacterial; fungicide; ophthalmological;
KW	analgesic; hypertensive; immunosuppressive; kinase inhibitor; kinase;
KW	cancer; peripheral nervous system; central nervous system;
KW	Alzheimer's disease; Parkinson's disease; multiple sclerosis;
KW	amyotrophic lateral sclerosis; viral infection; prion infection;
KW	ocular disease; migraine; pain; sexual dysfunction; mood disorder;
KW	attention disorder; cognition disorder; hypotension; hypertension;
KW	psychotic disorder; neurological disorder; dyskinesia;
KW	metabolic disorder; organ transplant rejection; enzyme.
XX	
OS	Homo sapiens.
XX	
XX	WO2003057841-A2.
FN	
XX	17-JUL-2003.
PD	
XX	31-DEC-2002; 2002WO-US041687.
FF	
XX	31-DEC-2001; 2001US-0343169P.
PR	
XX	(GRIG//) GRIGORIEV I V.
PA	(SUDA//) SUDARSANAM S.
XX	
XX	Grigoriev IV, Sudarsanam S;
PI	
XX	WPI; 2003-587115/55.
DR	
XX	New isolated, enriched or purified nucleic acid molecule encoding a
PT	kinase polypeptide, useful for treating cancer, immune-related diseases,
PT	cardiovascular disease, brain or neuronal-associated diseases and
PT	metabolic disorders.
XX	
XX	Claim 1; SEQ ID NO 80; 491pp; English.
PS	
XX	The invention relates to novel isolated, enriched or purified nucleic acid
CC	molecules encoding a kinase polypeptide. The nucleic acid molecule
CC	comprises a sequence that: (a) encodes a kinase polypeptide; (b) is a
CC	complement of (a); (c) hybridizes under stringent conditions to (a) and
CC	encodes a naturally occurring kinase polypeptide; (d) encodes the
CC	polypeptide in (a), except that it lacks one or more, but not all, of an
CC	N-terminal domain, C-terminal catalytic domain, a catalytic domain, a C-
CC	terminal tail; or (e) is a complement of (d). The nucleic acid molecules,
CC	polypeptides, methods and substance are useful for treating cancers, or
CC	immune-related diseases or disorders, cardiovascular disease, brain or
CC	neuronal-associated diseases, and metabolic disorders. The disorders are
CC	preferably cancers of the tissues or of hematopoietic origin, diseases of
CC	the central or peripheral nervous system, Alzheimer's disease,
CC	Parkinson's disease, multiple sclerosis, amyotrophic lateral sclerosis,
CC	viral infections, infections caused by prions, infections caused by
CC	bacteria, infections caused by fungi, ocular diseases, migraines, pain,
CC	sexual dysfunction, mood disorders, attention disorders, cognition
CC	disorders, hypotension, hypertension, psychotic disorders, neurological
CC	disorders, dyskinesias, metabolic disorders and organ transplant
CC	rejection. This sequence corresponds to one of the kinase polypeptides of
CC	the invention.
XX	
XX	Sequence 490 AA;
XX	
XX	Query Match 62.0%; Score 49; DB 7; Length 490;

Best Local Similarity 66.7%; Pred. No. 5.9;
Matches 10; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 RHYGETKMQRSRS 15
| | | | |
Db 240 RTVGATRLNQRSRS 254

RESULT 44
ADRI5692
ID ADR15692 standard; protein; 490 AA.
XX
AC ADR15692;
XX
DT 04-NOV-2004 (first entry)
XX
DE Kinase 730440 hCT1809245, SEQ ID 85.
XX
KW Cytostatic; Cardiovascular; Neuroprotective; Nootropic; Antiparkinsonian;
KW Virucide; Cerebroprotective; Antibacterial; Fungicide; Ophthalmological;
KW Antimigraine; Analgesic; Endocrine; Tranquillizer; Hypotensive;
KW Immunosuppressive; Gene Therapy; Kinase; enzyme; cancer;
KW Immune-related disease; cardiovascular disease;
KW neuronal-associated disease; metabolic disorder.
XX
OS Homo sapiens.
XX
PN WO2004069154-A2.
XX
PD 19-AUG-2004.
XX
PF 28-JAN-2003; 2003WO-US002234.
XX
PR 28-JAN-2003; 2003WO-US002234.
XX
PA (GRIG/) GRIGORIEV I V.
PA (SUDA/) SUDARSANAM S.
XX
PI Grigoriev IV, Sudarsanam S;
XX
DR WPI; 2004-604329/58.
DR N-PSDB; ADR15709.
XX
XX New isolated, enriched, or purified kinase nucleic acids and
PT polypeptides, useful for diagnosing or treating kinase-related diseases
PT and conditions, e.g. cardiovascular disease, brain or neuronal-associated
PT diseases, or metabolic disorders.
XX
PS Claim 7; Fig 2; 496pp; English.
XX
CC The present invention relates to a method for detecting remote
CC polypeptide homologues, comprising analysis of conserved secondary
CC structure pattern in a protein family, and conserved active site amino
CC acid residues. The analyses are used to identify conserved residues
CC embedded into the secondary structure pattern (CRISP), which are used to
CC detect remote homologues of the referent protein family, wherein said
CC referent protein family is the protein kinase family. The present
CC sequence is a kinase, used to illustrate the method of the invention. The
CC kinases are useful for diagnosing or treating various kinase-related
CC diseases and conditions. Diseases or disorders include cancers, immune-
CC related diseases and disorders, cardiovascular disease, brain or neuronal
CC -associated diseases, or metabolic disorders. Preferably, the diseases or
CC disorders are cancers of tissues, cancers of haematopoietic origin,
CC diseases of the central nervous system, diseases of the peripheral
CC nervous system, Alzheimer's disease, Parkinson's disease, multiple
CC sclerosis, amyotrophic lateral sclerosis, viral infections, infections
CC caused by prions, infections caused by bacteria, infections caused by
CC fungi, or ocular diseases. The disease or disorder is also migraines,
CC pain, sexual dysfunction, mood disorders, attention disorders, cognition
CC disorders, hypertension, psychotic disorders, neurological disorders,
CC dyskinesias, metabolic disorders, or organ transplant rejection.
XX
SQ Sequence 490 AA;

Query Match 62.0%; Score 49; DB 8; Length 490;
Best Local Similarity 66.7%; Pred. No. 5.9;
Matches 10; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 RHYGETKMQRSRS 15
| | | | |
Db 240 RTVGATRLNQRSRS 254

RESULT 45
ADC23340
ID ADC23340 standard; protein; 512 AA.
XX
AC ADC23340;
XX
DT 18-DEC-2003 (first entry)
XX
DE Human kinesin-like DNA binding protein (KID) (SeqID 4).
XX
KW human; enzyme; motor domain; kinesin-like DNA binding protein; KID;
KW cytosolic; cardiant; immunomodulator; antiinflammatory; gene therapy;
KW cancer; hyperplasia; restenosis; cellular proliferation disorder;
KW cardiac hypertrophy; immune disorder; inflammation.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Misc-difference 2
FT /note= "Encoded by CA"
XX
PN US6387644-B1.
XX
PD 14-MAY-2002.
XX
PF 28-NOV-2000; 2000US-00724224.
XX
PR 20-APR-1999; 99US-00295612.
PR 20-JUN-2000; 2000US-00597292.
XX
PA (CYTO-) CYTOKINETICS INC.
XX
PI Beraud C;
XX
DR WPI; 2003-706919/67.
DR N-PSDB; ADC23339.
XX
PT Identifying a candidate agent as modulator of function of a target
PT protein for treating cellular proliferation disorders by adding a
PT candidate agent to a mixture of the target protein that
PT directly/indirectly produces ADP or phosphate.
XX
PS Claim 1; SEQ ID NO 4; 26pp; English.
XX
CC This invention relates to a novel method for high throughput screening
CC systems used to identify compounds for the treatment of cellular
CC proliferation disorders. Specifically, it refers to candidate agents that
CC are capable of modulating the activity of target proteins having motor
CC domains, such that the target protein directly or indirectly produces ADP
CC or phosphate. Furthermore, this activity can be determined using
CC fluorescence or absorbance readouts. The present invention describes a
CC method that identifies modulators of the target protein, which is a
CC kinesin-like DNA binding protein (known as KID) as cytosolic, cardiants,
CC immunomodulators and antiinflammatory. Accordingly, through gene
CC therapy, they can be used for the treatment of cancer, hyperplasias,
CC restenosis, cardiac hypertrophy, immune disorders and inflammation. This
CC polypeptide sequence is human KID protein (SeqID 4) of the invention.
XX
SQ Sequence 512 AA;

Query Match 62.0%; Score 49; DB 7; Length 512;
Best Local Similarity 66.7%; Pred. No. 6.2;
Matches 10; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY	1	RHYGETKNQSSRS	15
Db	233	RTVGATRLNQSSRS	247
RESULT 47			
ID	ADQ88355	ADQ88355 standard; protein; 512 AA.	
XX	AC	ADQ88355;	
XX	DT	07-OCT-2004 (first entry)	
XX	DE	Human microtubule motor protein KID #2.	
XX	KW	Human; microtubule motor protein; cellular proliferative disorder; cancer; hyperplasia; restenosis; cardiac hypertrophy; immune disorder; wound; inflammation; autoimmune disease; arthritis; skin carcinoma; inflammatory bowel disease; solid tumour; testicular carcinoma; breast carcinoma; cervical carcinoma; testicular carcinoma; bronchogenic carcinoma; alveolar carcinoma; adenocarcinoma; osteogenic sarcoma; multiple myeloma; malignant melanoma; KID.	
XX	OS	Homo sapiens.	
XX	Key	Location/Qualifiers	
XX	FT	Misc-difference 2	
XX	FT	/note= "Encoded by CA"	
XX	PN	US2004142397-A1.	
XX	PD	22-JUL-2004.	
XX	PF	09-MAR-2004; 2004US-00797893.	
XX	PR	20-APR-1999; 99US-00295612.	
XX	PR	20-JUN-2000; 2000US-00597292.	
XX	PR	28-NOV-2000; 2000US-00724224.	
XX	PR	06-MAR-2002; 2002US-00093317.	
XX	XX	(CYTO-) CYTOKINETICS INC.	
XX	PA	Beraud C;	
XX	PI	WPI; 2004-552562/53.	
XX	DR	N-PSDB; ADQ88354.	
XX	XX	Novel isolated microtubule motor protein, useful for identifying candidate agent modulating function of protein, for treating cellular proliferative diseases such as cancer, restenosis, cardiac hypertrophy and inflammation.	
XX	PS	Claim 5; SEQ ID NO 4; 27pp; English.	
XX	XX	The invention relates to microtubule motor proteins and nucleic acid molecules encoding such proteins. Microtubule motor proteins are useful for identifying candidate agents modulating the function of protein which in turn are useful for treating cellular proliferative disorders such as cancer, hyperplasia, restenosis, cardiac hypertrophy, immune disorders, wounds and inflammation. Other disorders treated include autoimmune disease, arthritis, inflammatory bowel disease, solid tumours such as skin carcinomas, breast carcinomas, cervical carcinomas, testicular carcinomas, bronchogenic carcinoma, alveolar carcinoma, adenocarcinoma, tumour of bone such as osteogenic sarcoma, multiple myeloma, malignant melanoma etc. The present sequence is a human microtubule motor protein KID polypeptide.	
XX	SQ	Sequence 512 AA;	
Query Match 62.0%; Score 49; DB 8; Length 512;			
Best Local Similarity 66.7%; Pred. No. 6.2;			
Matches 10; Conservative 2; Mismatches 3; Indels 0; Gaps 0;			

QY	1	RHYGETKNQSSRS	15
Db	233	RTVGATRLNQSSRS	247
RESULT 46			
ID	ADQ60230	ADQ60230 standard; protein; 512 AA.	
XX	AC	ADQ60230;	
XX	DT	23-SEP-2004 (first entry)	
XX	DE	Human microtubule motor protein #2.	
XX	KW	Human; microtubule motor protein; cellular proliferation disorder; cancer; hyperplasia; restenosis; cardiac hypertrophy; immune disorder; inflammation; kinesin-like DNA binding protein; KID; autoimmune disease; arthritis; graft rejection; inflammatory bowel disease; angioplasty.	
XX	OS	Homo sapiens.	
XX	PN	US6762043-B1.	
XX	PD	13-JUL-2004.	
XX	PF	06-MAR-2002; 2002US-00093317.	
XX	PR	20-APR-1999; 99US-00295612.	
XX	PR	20-JUN-2000; 2000US-00597292.	
XX	PR	28-NOV-2000; 2000US-00724224.	
XX	PA	(CYTO-) CYTOKINETICS INC.	
XX	PI	Beraud C;	
XX	DR	WPI; 2004-532491/51.	
XX	PT	New isolated microtubule motor protein, useful for screening modulators for treating cellular proliferation disorders such as cancer, hyperplasias, restenosis, cardiac hypertrophy, immune disorders and inflammation.	
XX	PS	Claim 1; SEQ ID NO 4; 26pp; English.	
XX	CC	The invention relates to human microtubule motor proteins and the nucleic acids encoding them. The invention also relates to a method of screening for modulators of a motor protein which has microtubule stimulated ATPase activity, a method of testing for ATPase activity of microtubule motor proteins, methods to identify candidate agents that bind to a target protein or act as a modulator of the binding characteristics or biological activity of a target protein, modulators of the target protein, and methods of treating cellular proliferation disorders such as cancer, hyperplasias, restenosis, cardiac hypertrophy, immune disorders and inflammation, for treating disorders associated with kinesin-like DNA binding protein (KID) and for inhibiting KID. The sequences are used for screening for modulators of motor proteins useful for treating cellular proliferation disorders such as cancer, hyperplasias, restenosis, cardiac hypertrophy, immune disorders and inflammation, for treating disorders associated with KID and for inhibiting KID and for treating autoimmune diseases, arthritis, graft rejection, inflammatory bowel disease and proliferation induced after medical procedures including surgery and angioplasty. This sequence represents a human microtubule motor protein of the invention. Note: The specification states that this sequence is encoded by the nucleic acid featured as SEQ ID NO:3, but this does not appear to be the case.	
XX	SQ	Sequence 512 AA;	
Query Match 62.0%; Score 49; DB 8; Length 512;			
Best Local Similarity 66.7%; Pred. No. 6.2;			
Matches 10; Conservative 2; Mismatches 3; Indels 0; Gaps 0;			

The invention relates to human tumour-associated antigenic target (TAT) polypeptides, and their related nucleic acids. The TAT polypeptides are overexpressed in cancer tissues compared to normal tissues, and may thus serve as effective targets for the diagnosis and treatment of cancer in mammals. The invention also relates to nucleic acid and polypeptide sequences at least 80% identical to the TAT nucleic acids and polypeptides; expression vectors and host cells comprising a TAT nucleic acid; an antibody specific for a TAT polypeptide; a peptide or organic molecule which binds to a TAT polypeptide; fusion proteins comprising a TAT polypeptide; and methods and compositions for the treatment or diagnosis of cancer in mammals. TAT polypeptides, nucleic acids, antibodies, antagonists, binding molecules and compositions are useful for diagnosing or treating a cell proliferative disorder associated with increased TAT expression, particularly cancers such as breast cancer, colorectal cancer, lung cancer, ovarian cancer, liver cancer, bladder cancer, pancreatic cancer, cervical cancer, cancers of the central nervous system, melanoma and leukaemia. TAT nucleic acids may further be used as hybridisation probes, in chromosome and gene mapping, in chromosome identification and in gene therapy. The present sequence represents a TAT polypeptide of the invention.

Sequence 665 AA;

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XX
SQ      Sequence 665 AA;
        Query Match      62.0%;      Score 49;  DB 8;  Length 665;
        Best Local Similarity 66.7%;  Pred. NO. 8.2;
        Matches 10;  Conservative 2;  Mismatches 3;  Indels 0;  Gaps 0;

Qy      1 RHYGETKNQRRSSR 15
Db      232 RTVGATRLNQRRSSR 246

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XX	RESULT 50
AD	ADZ13122 standard; protein; 2033 AA.
XX	ADZ13122
XX	ADZ13122;
XX	16-JUN-2005 (first entry)
XX	Murine cancer-associated protein #70.
DE	
XX	Diagnosis; DNA microarray; microarray; biochip; cancer; neoplasm;
KW	Cytostatic.
KW	
XX	Mus sp.
OS	
XX	WO2005031001-A2.
FN	
XX	07-APR-2005.
PD	
XX	
XX	23-SEP-2004; 2004WO-US031617.
PF	
XX	
XX	23-SEP-2003; 2003US-00659920.
PR	
XX	(CHIR) CHIRON CORP.
PA	
PI	Morris DW, Malandro MS;
XX	
XX	WPI; 2005-273395/28.
DR	N-PSDB; ADZ13121.
XX	
XX	Nucleic acid array useful for detecting cancer associated nucleic acid,
PT	comprises two or more nucleic acid probes.
PT	
XX	
XX	Disclosure; SEQ ID NO 642; 198pp; English.
PS	
XX	
XX	The invention relates to a nucleic acid array for detecting a cancer
CC	associated (CA) nucleic acid, comprising two or more nucleic acid probes.
CC	The invention also relates to a peptide array comprising two or more
CC	isolated polypeptides encoded by a CA nucleic acid sequence, a compound
CC	that binds to a polypeptide, an isolated antibody or its fragment which

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OM protein - protein search, using sw model

Run on: April 21, 2006, 13:38:26 ; Search time 38 Seconds
(without alignments)
37.980 Million cell updates/sec

Title: US-09-993-399-1

Perfect score: 79

Sequence: 1 RHYGKMNQRSSRS 15

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1000 summaries

Database :

PIR 80:*

1: pir1:*

2: pir2:*

3: pir3:*

4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	79	100.0	2663	1 S28261	centromere protein
2	69	87.3	2954	2 T14156	kinesin-related pr
3	58	73.4	823	2 T52425	kinesin-like prote
4	58	73.4	888	2 D95619	protein T30846.9 [
5	54	68.4	955	2 A47334	LcKin kinesin-rela
6	51	64.6	581	2 F84599	probable kinesin h
7	51	64.6	834	2 T06055	hypothetical prote
8	50	63.3	1459	2 T30196	kinesin motor prot
9	49	62.0	198	2 E86183	hypothetical prote
10	49	62.0	665	2 S62328	kinesin-like DNA b
11	48	60.8	1070	2 T06733	kinesin homolog F2
12	47	59.5	670	2 T29898	kinesin protein OS
13	47	59.5	672	2 S54351	kinesin osm-3 - Ca
14	47	59.5	754	2 S48020	kinesin-related pr
15	47	59.5	793	2 S34830	kinesin-related pr
16	46	58.2	102	2 E85814	hypothetical prote
17	46	58.2	108	2 E90966	hypothetical prote
18	46	58.2	127	2 G64960	probable membrane
19	46	58.2	932	2 T49235	kinesin-like prote
20	45	57.0	143	2 C44259	kinesin heavy chai
21	45	57.0	315	2 AF1393	glycosyl transfera
22	45	57.0	315	2 A11768	glycosyl transfera
23	45	57.0	777	2 C85065	kinesin-like prote
24	45	57.0	963	1 A41919	kinesin heavy chai
25	45	57.0	967	1 A31497	kinesin heavy chai
26	45	57.0	975	1 A31497	kinesin heavy chai
27	45	57.0	1027	2 S37711	kinesin heavy chai
28	45	57.0	1031	1 A38713	kinesin heavy chai
29	45	57.0	1032	2 I38510	neuronal kinesin h

30	44	55.7	294	2 S38983	kinesin-related pr
31	44	55.7	706	1 C42640	kinesin-related pr
32	44	55.7	742	1 S58691	protein kinesin F2
33	44	55.7	987	2 B96766	hypothetical prote
34	44	55.7	1130	2 T21134	kinesin-like prote
35	43	54.4	332	2 C48835	kinesin-related pr
36	43	54.4	701	1 B44259	kinesin-related pr
37	43	54.4	747	1 A57107	kinesin homolog KH
38	43	54.4	786	2 A53939	hypothetical prote
39	43	54.4	968	2 T45746	kinesin-like prote
40	43	54.4	1056	2 C96661	hypothetical prote
41	43	54.4	1263	2 T13465	hypothetical prote
42	42	53.2	699	1 S38982	kinesin-related pr
43	42	53.2	861	2 T00434	probable kinesin h
44	41	51.9	573	2 F26691	probable fumarate
45	41	51.9	770	1 A44337	kinesin-related pr
46	41	51.9	832	2 T38749	kinesin-like prote
47	41	51.9	1265	2 T03792	kinesin-related pr
48	41	51.9	1265	2 T07397	kinesin heavy chai
49	40	50.6	202	2 D85058	hypothetical prote
50	40	50.6	219	2 A75088	hypothetical prote
51	40	50.6	535	2 S56147	GCN20-2 protein -
52	40	50.6	784	1 A55236	kinesin-related pr
53	40	50.6	1075	2 T45570	kinesin-like prote
54	40	50.6	1142	2 S59359	GIN4 protein - yea
55	39.5	50.0	738	2 S32372	transforming prote
56	39	49.4	447	2 S76033	hypothetical prote
57	39	49.4	793	2 JC5831	kinesin-related pr
58	39	49.4	885	1 T04321	endopeptidase La h
59	39	49.4	921	2 T01775	hypothetical prote
60	39	49.4	928	2 T10164	kinesin heavy chai
61	39	49.4	929	2 T51932	kinesin [imported]
62	39	49.4	932	2 T30099	hypothetical prote
63	39	49.4	987	2 T51360	kinesin-like heavy
64	39	49.4	1022	2 E84792	probable kinesin h
65	39	49.4	1038	1 B42641	kinesin-related pr
66	38.5	48.7	1083	2 T36844	hypothetical prote
67	38	48.1	1221	2 T06815	probable embryonic
68	38	48.1	324	2 D81452	3-oxoacyl-lacetyl-ca
69	38	48.1	325	2 S32908	hypothetical prote
70	38	48.1	330	2 B48835	kinesin-like prote
71	38	48.1	351	2 T40896	hypothetical prote
72	38	48.1	365	2 T50566	probable ABC-type
73	38	48.1	404	2 A34919	type II site-speci
74	38	48.1	692	2 T47493	hypothetical prote
75	38	48.1	718	2 A82352	iron(III) compound
76	38	48.1	857	2 E84600	probable kinesin h
77	38	48.1	873	2 JC7079	homeobox protein z
78	38	48.1	873	2 JC4863	homeobox protein z
79	38	48.1	888	2 T01081	hypothetical prote
80	38	48.1	1006	2 T02017	kinesin-related pr
81	38	48.1	1032	2 B86224	hypothetical prote
82	38	48.1	1058	2 T47525	kinesin-related pr
83	38	48.1	1076	2 B84687	probable kinesin-1
84	38	48.1	1304	2 C85188	disease resistance
85	38	48.1	1388	2 T30335	KLP2 protein - Afr
86	37	46.8	159	1 JIMS	ig J chain precurs
87	37	46.8	182	2 S33990	finger protein ZNF
88	37	46.8	329	2 S73345	sn-glycerol-3-phos
89	37	46.8	470	2 S02068	RNA-directed RNA p
90	37	46.8	507	2 T08337	hypothetical prote
91	37	46.8	575	2 T48224	probable homeodoma
92	37	46.8	596	2 AB1047	succinate dehydrog
93	37	46.8	602	1 RDECFP	fumarate reductase
94	37	46.8	602	2 G86111	flavoprotein subun
95	37	46.8	602	2 G91270	flavoprotein subun
96	37	46.8	899	2 S76449	hypothetical prote
97	37	46.8	909	2 H86350	hypothetical prote
98	37	46.8	960	2 A71420	pyruvate, phosphat
99	37	46.8	1056	2 H84777	probable kinesin-r
100	37	46.8	1121	2 T06065	hypothetical prote
101	37	46.8	1195	2 B96745	probable kinesin T
102	37	46.8	1619	2 T18499	hypothetical prote

103	37	45.8	1893	2	T22661	hypotheical prote	176	35	44.3	1150	1	A55289	kinesin-like prote
104	36	45.6	101	2	T14706	probable C-type na	177	35	44.3	1225	2	A56514	chromokinesin - ch
105	36	45.6	139	2	I40783	hypotheical prote	178	35	44.3	1226	2	I51617	kinesin-like prote
106	36	45.6	168	2	S47467	dihydrofolate redu	179	35	44.3	1229	2	T48959	kinesin-like prote
107	36	45.6	182	2	I40175	signal peptidase I	180	35	44.3	1231	2	A54803	microtubule-associ
108	36	45.6	199	2	A13206	transcription regu	181	35	44.3	1650	2	S28721	hypotheical prote
109	36	45.6	202	2	T22914	hypotheical prote	182	35	44.3	1695	2	A56921	kinesin family pro
110	36	45.6	204	2	A13396	hypotheical prote	183	35	44.3	1958	2	T39808	hypotheical prote
111	36	45.6	204	2	A13771	hypotheical prote	184	35	44.3	2279	2	T42531	acetyl-CoA carboxy
112	36	45.6	214	2	S49599	probable permease	185	35	44.3	2280	2	T39306	acetyl-CoA carboxy
113	36	45.6	248	2	H70511	probable prCA prot	186	35	44.3	2359	2	T03094	A-kinase anchor pr
114	36	45.6	265	2	E87074	proteasome [alpha]	187	35	44.3	2437	2	T18482	hypotheical prote
115	36	45.6	300	2	S72865	hypotheical prote	188	35	44.3	56	2	AF0717	DNA-binding protei
116	36	45.6	330	2	E71534	probable pbp2b met	189	34	43.0	90	2	H82343	transforming protei
117	36	45.6	330	2	E90578	30S ribosomal prot	190	34	43.0	109	1	TVHUSE	phospholipase A2 (
118	36	45.6	344	2	T33057	hypotheical prote	191	34	43.0	139	2	JN0426	probable merf-fam1
119	36	45.6	375	2	T08134	oleosin-like prote	192	34	43.0	150	2	T36235	lysophospholipase
120	36	45.6	384	2	A47479	heparin lyase (EC	193	34	43.0	152	2	JN0427	probable transcrip
121	36	45.6	401	2	C87101	probable secreted	194	34	43.0	202	2	E95883	probable transcrip
122	36	45.6	411	1	S37643	protein kinase MSK	195	34	43.0	227	2	G89807	exotoxin 14 [impor
123	36	45.6	447	2	B64152	conserved hypothe	196	34	43.0	246	2	S75813	UDP-N-acetyl-D-man
124	36	45.6	513	2	A52504	hypotheical prote	197	34	43.0	260	1	B26325	deoxyribonuclease
125	36	45.6	519	2	IA54523	kinesin-related pr	198	34	43.0	272	2	A71618	merozoite surface
126	36	45.6	583	2	A82430	nitrate/nitrite se	199	34	43.0	275	2	S77009	hypotheical prote
127	36	45.6	622	2	A57281	kinesin-like motor	200	34	43.0	282	1	NDB0A	deoxyribonuclease
128	36	45.6	881	2	I84737	kinesin heavy chai	201	34	43.0	286	2	T09704	probable arginine/
129	36	45.6	915	2	H82104	cation transport A	202	34	43.0	290	2	T15374	hypotheical prote
130	36	45.6	1307	2	G96711	unknown protein, 9	203	34	43.0	298	2	T22250	hypotheical prote
131	36	45.6	1662	1	H71402	probable kinesin -	204	34	43.0	302	2	E83441	conserved hypothe
132	36	45.6	1743	2	T26859	hypotheical prote	205	34	43.0	313	2	E82762	conserved hypothe
133	36	45.6	1780	2	T17272	hypotheical prote	206	34	43.0	328	2	H81201	conserved hypothe
134	35.5	44.9	294	2	D85036	hypotheical prote	207	34	43.0	347	2	T06671	hypotheical prote
135	35.5	44.9	451	2	T15718	hypotheical prote	208	34	43.0	368	2	S39198	SASP degradation s
136	35	44.3	92	2	G84933	DNA-binding protei	209	34	43.0	372	1	A32375	L-selectin precurs
137	35	44.3	126	2	H89826	hypotheical prote	210	34	43.0	375	2	B11842	carbamoyl-phosphat
138	35	44.3	129	2	F82515	conserved hypothe	211	34	43.0	375	2	S62606	semenclostin - mous
139	35	44.3	147	2	E44259	kinesin-related pr	212	34	43.0	376	2	S36535	E2 protein - human
140	35	44.3	165	2	D86784	hypotheical prote	213	34	43.0	380	2	C90119	hypotheical prote
141	35	44.3	218	2	D86768	dihydrofolate redu	214	34	43.0	380	2	AG2620	hemolysin [impor
142	35	44.3	221	2	C37390	transfer protein T	215	34	43.0	384	2	G97402	hemolysin U97482 (
143	35	44.3	232	2	E89472	protein ZC53.6 [im	216	34	43.0	402	2	F82473	hypotheical prote
144	35	44.3	317	1	E87185	3',5'-cyclic-nucle	217	34	43.0	409	2	F70387	deoxyguanosinetrip
145	35	44.3	318	2	T35457	probable insertion	218	34	43.0	495	2	B71360	collagenase - Aqu
146	35	44.3	354	2	C96600	protein F14J16.16	219	34	43.0	502	2	UC8025	hypotheical prote
147	35	44.3	363	2	AE1837	hypotheical prote	220	34	43.0	545	2	F64579	cytochrome P450 en
148	35	44.3	372	2	JC5377	L-selectin precurs	221	34	43.0	545	2	F71932	site-specific DNA-
149	35	44.3	372	2	S23936	hypotheical prote	222	34	43.0	587	2	T29324	type II DNA modifi
150	35	44.3	384	2	F96601	hypotheical prote	223	34	43.0	599	2	T18316	hypotheical prote
151	35	44.3	408	2	S33683	site-specific DNA-	224	34	43.0	638	2	P95399	protein [imported
152	35	44.3	412	1	S37642	protein kinase MSK	225	34	43.0	666	1	A36026	kinesin-related pr
153	35	44.3	463	2	D97814	chromosomal replic	226	34	43.0	666	1	A36026	hypotheical prote
154	35	44.3	463	2	C71665	chromosomal replic	227	34	43.0	786	2	A96956	ATP-dependent prot
155	35	44.3	478	2	G90514	nadh oxidase (noxa	228	34	43.0	875	2	T09142	endopeptidase La h
156	35	44.3	493	2	S32037	finger protein XFG	229	34	43.0	885	2	D86151	F22M8.8 protein -
157	35	44.3	506	2	T08927	probable protein k	230	34	43.0	893	2	T35014	probable regulator
158	35	44.3	529	2	A24031	genome polyprotein	231	34	43.0	898	2	T21179	hypotheical prote
159	35	44.3	554	2	T50118	kinesin-related pr	232	34	43.0	944	2	A89624	protein F21A10.2 (
160	35	44.3	563	2	A69335	succinate dehydrog	233	34	43.0	944	2	S26710	spindle pole body
161	35	44.3	571	2	C70353	hypotheical prote	234	34	43.0	953	2	I48078	Chol antigen - Chi
162	35	44.3	623	2	T06704	numb-binding prote	235	34	43.0	960	1	S28262	kinesin-related pr
163	35	44.3	628	2	T09458	hypotheical prote	236	34	43.0	962	1	D70661	probable membran
164	35	44.3	716	1	A44259	kinesin-related pr	237	34	43.0	968	2	T51933	kinesin motor prot
165	35	44.3	728	2	T09457	probable lipoprote	238	34	43.0	1001	2	G87385	TonB-dependent rec
166	35	44.3	744	2	T06048	kinesin heavy chai	239	34	43.0	1233	2	T37045	nitrate reductase
167	35	44.3	760	2	S62792	pyruvate dehydrog	240	34	43.0	1285	2	H85041	hypotheical prote
168	35	44.3	843	2	G34868	mitotic checkpoint	241	34	43.0	1285	2	H85041	protein-tyrosine-p
169	35	44.3	882	2	G83018	probable kinesin h	242	34	43.0	2294	2	I67630	genome polyprotein
170	35	44.3	1058	2	T30178	probable kinesin h	243	34	43.0	2332	1	GNNYF	cell surface antig
171	35	44.3	1068	2	F84614	probable Pro-X car	244	34	43.0	2450	2	S71625	protein-tyrosine-p
172	35	44.3	1080	2	T19048	probable mitotic c	245	34	43.0	2466	2	I67629	protein-tyrosine-p
173	35	44.3	1102	2	T31004	kinesin-related pr	246	34	43.0	2490	1	A54971	protein-tyrosine-p
174	35	44.3	1121	2	T13796	hypotheical prote	247	34	43.0	2649	2	T51023	hypotheical prote
175	35	44.3	1121	2	T13750	hypotheical prote	248	34	43.0	2649	2	T51023	hypotheical prote

249	33.5	42.4	131	2	AG1421	hypothetical prote	322	33	41.8	566	2	C91045	nitrate/nitrite se
250	33.5	42.4	279	2	C82915	ribosomal prote	323	33	41.8	575	2	S46692	hypothetical prote
251	33.5	42.4	323	1	S03702	L-selectin precurs	324	33	41.8	604	2	A46150	proteoglycan-endo
252	33.5	42.4	385	1	A34015	serine transporter	325	33	41.8	607	2	AH0044	succinate dehydrog
253	33.5	42.4	417	2	D82172	late competence pr	326	33	41.8	611	2	T44962	hypothetical prote
254	33.5	42.4	439	2	A11388	probable transcrip	327	33	41.8	632	2	T32454	lipase precursor -
255	33.5	42.4	848	2	S48273	chromosome segrega	328	33	41.8	641	2	A24075	kinesin-related pr
256	33.5	42.4	1208	2	AE1947	hypothetical prote	329	33	41.8	671	2	T10755	sensory transducti
257	33	41.8	71	2	AG2418	transcription regu	330	33	41.8	700	2	E69146	ribonucleoside-tri
258	33	41.8	110	1	S70466	aspartate 1-decarb	331	33	41.8	707	1	A64047	hypothetical prote
259	33	41.8	124	1	A70343	DNA-binding protei	332	33	41.8	715	2	T33573	assimilatory nitra
260	33	41.8	136	2	E64067	protein kinase (EC	333	33	41.8	743	2	G83726	related to tol pro
261	33	41.8	137	2	T07891	protein kinase clk	334	33	41.8	756	2	T49475	hypothetical prote
262	33	41.8	139	2	S53638	plasmid stabilizat	335	33	41.8	771	2	S25814	hypothetical prote
263	33	41.8	142	2	H82660	lipopolysaccharide	336	33	41.8	772	2	T26330	outer membrane uhn
264	33	41.8	161	2	B70323	prophage p12 prote	337	33	41.8	802	1	A37142	hypothetical prote
265	33	41.8	198	2	G86754	probable glycosida	338	33	41.8	825	2	T29634	endopeptidase Clp
266	33	41.8	203	2	AH0223	hypothetical prote	339	33	41.8	867	2	D71555	meloidia-specific p
267	33	41.8	204	2	C83038	nodulin-26b - soyb	340	33	41.8	878	2	A55201	hypothetical prote
268	33	41.8	213	2	B25750	hypothetical prote	341	33	41.8	906	2	A82533	hypothetical prote
269	33	41.8	221	2	T29468	hypothetical prote	342	33	41.8	931	2	H86387	hypothetical prote
270	33	41.8	225	2	S50458	hypothetical prote	343	33	41.8	934	2	G91198	Gamma intimin [imp
271	33	41.8	236	2	B85025	hypothetical prote	344	33	41.8	934	2	C86045	intimin adherence
272	33	41.8	258	2	S55036	tyrosine-rich hydr	345	33	41.8	935	1	I41193	outer membrane pro
273	33	41.8	262	1	A26324	deoxyribonuclease	346	33	41.8	936	1	I40705	bacterial adhesin
274	33	41.8	265	2	T05668	pollen allergen ho	347	33	41.8	939	2	I41197	eee protein (enter
275	33	41.8	273	2	D71436	hypothetical prote	348	33	41.8	958	2	T20621	hypothetical prote
276	33	41.8	281	2	AC2138	hypothetical prote	349	33	41.8	1024	2	T34517	kinesin-related pr
277	33	41.8	284	1	JC2526	deoxyribonuclease	350	33	41.8	1073	2	S14032	kinesin-like prote
278	33	41.8	284	2	JC8053	deoxyribonuclease	351	33	41.8	1085	2	T38378	kinesin-like prote
279	33	41.8	288	2	S68798	RNA-binding protei	352	33	41.8	1089	2	T21582	hypothetical prote
280	33	41.8	290	2	A86281	protein Fl0B6.4 [i	353	33	41.8	1112	2	S49432	replicase 126K - o
281	33	41.8	312	2	PH0224	class-3 porin prot	354	33	41.8	1184	1	A34795	kinesin-related pr
282	33	41.8	313	2	JH0254	hypothetical prote	355	33	41.8	1201	2	T00444	hypothetical prote
283	33	41.8	314	2	T43132	hypothetical prote	356	33	41.8	1210	2	A25547	ice nucleation pro
284	33	41.8	321	2	T16451	hypothetical prote	357	33	41.8	1218	2	T30447	probable helicase
285	33	41.8	322	2	AE3359	lipic acid synthe	358	33	41.8	1236	2	B36329	hypothetical prote
286	33	41.8	330	2	AG0309	probable LacI-fami	359	33	41.8	1254	2	T18277	kinesin heavy chai
287	33	41.8	331	2	A10534	hypothetical prote	360	33	41.8	1256	2	C71436	probable resistanc
288	33	41.8	337	2	AD0608	probable oxidoredu	361	33	41.8	1317	2	B85189	disease resistance
289	33	41.8	338	2	AE1119	oxidoreductase hom	362	33	41.8	1325	2	T01037	hypothetical prote
290	33	41.8	344	2	AH1479	oxidoreductase hom	363	33	41.8	1495	2	T48429	hypothetical prote
291	33	41.8	348	2	S61037	hypothetical prote	364	33	41.8	1549	2	T13940	ankyrin - fruit fl
292	33	41.8	349	2	D64825	hypothetical prote	365	33	41.8	1576	2	T29237	hypothetical prote
293	33	41.8	349	2	B90748	hypothetical prote	366	33	41.8	1584	1	JN0114	kinesin-related pr
294	33	41.8	349	2	F85598	hypothetical prote	367	33	41.8	1584	2	T15822	kinesin-like prote
295	33	41.8	360	2	S48365	hypothetical prote	368	33	41.8	1742	2	T49451	kinesin-like prote
296	33	41.8	373	2	T47115	probable 4-carboxy	369	33	41.8	1921	2	T13827	kinesin-73 - fruit
297	33	41.8	392	2	F83381	probable molybdopt	370	33	41.8	2215	2	T16871	hypothetical prote
298	33	41.8	397	2	T04206	hypothetical prote	371	33	41.8	2336	2	S37077	genome polyprotein
299	33	41.8	402	2	C71440	hypothetical prote	372	33	41.8	2467	2	D71437	probable resistanc
300	33	41.8	419	2	B49418	spermatogenesis fa	373	33	41.8	4717	2	T41581	hypothetical coile
301	33	41.8	437	2	S67679	probable membrane	374	32.5	41.1	88	2	H89858	conserved hypotet
302	33	41.8	464	2	S45363	LEO1 protein - yea	375	32.5	41.1	331	2	F85873	cell division prot
303	33	41.8	470	2	A94999	metalloelastase HM	376	32.5	41.1	331	2	E51029	cell division prot
304	33	41.8	473	2	S53119	RNA-directed RNA p	377	32.5	41.1	331	2	G65004	Div protein - Esch
305	33	41.8	482	2	H97348	NADP-dependent gly	378	32.5	41.1	352	2	T39363	RNA binding protei
306	33	41.8	493	2	G83564	probable ATPase PA	379	32.5	41.1	439	2	AC1764	late competence pr
307	33	41.8	496	2	A49418	spermatogenesis fa	380	32.5	41.1	477	2	S76496	hypothetical prote
308	33	41.8	499	2	S53637	protein kinase clk	381	32.5	41.1	718	2	A13420	penicillin-binding
309	33	41.8	507	2	T45825	hypothetical prote	382	32.5	41.1	1130	2	T30251	repetin - mouse
310	33	41.8	511	2	AH1225	cobyrbic acid synth	383	32.5	41.1	2541	2	T29340	hypothetical prote
311	33	41.8	513	2	G96757	probable protein A	384	32	40.5	42	2	A71265	hypothetical prote
312	33	41.8	527	2	AE2380	type I restriction	385	32	40.5	57	2	H72592	probable aerolysin
313	33	41.8	527	2	T41856	AckNPV orf119 - Bo	386	32	40.5	64	2	T05933	probable 3-methyl-
314	33	41.8	534	2	S76219	hypothetical prote	387	32	40.5	67	2	AC1037	probable phage tai
315	33	41.8	542	2	JH1524	O-succinylthiomseri	388	32	40.5	67	2	AG0927	probable phage tai
316	33	41.8	543	2	H84724	probable ARI-like	389	32	40.5	76	2	G90957	probable derepress
317	33	41.8	562	2	A44944	apical membrane an	390	32	40.5	76	2	H85805	unknown protein en
318	33	41.8	563	2	A39238	66K merozoite surf	391	32	40.5	76	2	AD2538	hypothetical prote
319	33	41.8	566	2	AD0816	nitrate/nitrite se	392	32	40.5	96	2	B75114	hypothetical prote
320	33	41.8	566	2	F85889	hypothetical prote	393	32	40.5	100	2	E83037	urease gamma subun
321	33	41.8	566	2	D65022	nitrate/nitrite se	394	32	40.5	107	2	PH0971	Ig heavy chain V r

395	32	40.5	119	2	F30502	Ig heavy chain V r	468	32	40.5	466	2	A86033	probable permease
396	32	40.5	136	2	T03292	probable signal re	469	32	40.5	468	2	T08139	shaggy-like protei
397	32	40.5	136	2	T46345	hypothetical prote	470	32	40.5	472	1	T01236	serine/threonine-s
398	32	40.5	137	2	H32513	Ig heavy chain pre	471	32	40.5	472	1	T12955	probable protein k
399	32	40.5	137	2	T49243	hypothetical prote	472	32	40.5	477	2	JE0343	tear protein - rat
400	32	40.5	138	2	B70941	hypothetical prote	473	32	40.5	485	2	E81871	probable GTP-bind
401	32	40.5	149	2	H70441	hypothetical prote	474	32	40.5	485	2	G81149	essential GTPase N
402	32	40.5	152	2	A10448	ribosomal protein	475	32	40.5	491	2	I40455	penicillin binding
403	32	40.5	159	2	B70063	probable ribonucle	476	32	40.5	505	2	C69666	NADH dehydrogenase
404	32	40.5	177	2	F96739	hypothetical prote	477	32	40.5	511	1	B34160	cytochrome P450 4A
405	32	40.5	188	2	H81066	hypothetical prote	478	32	40.5	515	2	JC1525	alpha-1B-adrenerg
406	32	40.5	191	2	G81268	hypothetical prote	479	32	40.5	517	2	A45121	alpha-1B adrenerg
407	32	40.5	196	2	S41281	50S ribosomal prot	480	32	40.5	523	2	A53196	orphan hormone nuc
408	32	40.5	196	2	S41282	ribosomal protein	481	32	40.5	527	1	S69203	teichoic acid tran
409	32	40.5	196	2	S41254	ribosomal protein	482	32	40.5	532	2	JC6170	GATA-transcription
410	32	40.5	196	2	S41255	ribosomal protein	483	32	40.5	534	2	T01500	cytokinin oxidase
411	32	40.5	196	2	S41266	ribosomal protein	484	32	40.5	534	2	T51929	cytokinin oxidase
412	32	40.5	196	2	S41278	ribosomal protein	485	32	40.5	547	2	A56575	puff-specific nucl
413	32	40.5	196	2	S41276	ribosomal protein	486	32	40.5	562	2	JU0033	hypothetical L1 pr
414	32	40.5	196	2	S41283	ribosomal protein	487	32	40.5	571	2	S49119	embryonic/neonatal
415	32	40.5	196	2	S41284	ribosomal protein	488	32	40.5	572	2	S73730	MG307 homolog H08
416	32	40.5	199	2	T23484	hypothetical prote	489	32	40.5	574	2	B83388	probable carbamoyl
417	32	40.5	201	1	R3R24	ribosomal protein	490	32	40.5	577	2	D97337	mismatch repair pr
418	32	40.5	201	1	R3R24	ribosomal protein	491	32	40.5	595	2	T31077	probable ABC-trans
419	32	40.5	201	1	H85910	unknown protein en	492	32	40.5	605	2	D83007	regulatory protein
420	32	40.5	216	2	D97315	metallo-beta-lacta	493	32	40.5	614	2	B86461	probable protein k
421	32	40.5	233	2	H97094	hypothetical prote	494	32	40.5	616	2	A36094	diphosphate-fructo
422	32	40.5	237	2	S55614	hypothetical prote	495	32	40.5	621	2	JC7892	acyl-CoA dehydrog
423	32	40.5	244	2	T15996	hypothetical prote	496	32	40.5	621	2	I49199	growth factor rece
424	32	40.5	244	2	T41030	hypothetical prote	497	32	40.5	622	2	E83160	two-component sens
425	32	40.5	257	2	S56815	hypothetical prote	498	32	40.5	625	2	S69707	hypothetical prote
426	32	40.5	263	2	F82311	hypothetical prote	499	32	40.5	640	2	A64065	hypothetical prote
427	32	40.5	263	2	AF0420	survival protein S	500	32	40.5	648	2	AF2257	hypothetical prote
428	32	40.5	266	2	T02807	phosphonates trans	501	32	40.5	666	2	T22943	hypothetical prote
429	32	40.5	268	2	S03328	arsenate reductase	502	32	40.5	668	2	T02791	mitotic centromere
430	32	40.5	268	2	S04135	embryonic abundant	503	32	40.5	673	2	S60173	fragile X mental r
431	32	40.5	268	2	S04136	embryonic abundant	504	32	40.5	693	2	S46417	heat shock protein
432	32	40.5	268	2	S05471	embryonic abundant	505	32	40.5	695	2	G85135	hypothetical prote
433	32	40.5	268	2	S14068	seed protein precu	506	32	40.5	700	1	S09748	kinesin-related pr
434	32	40.5	274	2	D95339	hypothetical prote	507	32	40.5	705	2	T01730	hypothetical prote
435	32	40.5	287	2	A27082	2,4-dichlorophenox	508	32	40.5	707	1	LEEBBV	hemolysin secretio
436	32	40.5	290	2	T24747	hypothetical prote	509	32	40.5	713	2	I25114	ABC transporter At
437	32	40.5	296	2	T29923	hypothetical prote	510	32	40.5	714	2	D85014	hypothetical prote
438	32	40.5	302	2	AC2225	hypothetical prote	511	32	40.5	720	2	H95321	alpha-galactosidas
439	32	40.5	305	2	S77397	yabc protein homol	512	32	40.5	720	2	G98085	alpha-galactosidas
440	32	40.5	308	1	G64306	glutaminase homolo	513	32	40.5	725	2	S57127	hypothetical prote
441	32	40.5	308	2	C90895	probable glutamina	514	32	40.5	747	2	T23607	probable membrane
442	32	40.5	308	2	E85722	probable glutamina	515	32	40.5	755	2	E97080	hypothetical prote
443	32	40.5	309	2	T15696	hypothetical prote	516	32	40.5	757	2	AC2691	uVRA-like protein,
444	32	40.5	326	2	T05094	peroxidase homolog	517	32	40.5	757	2	G97472	penicillin binding
445	32	40.5	331	2	S76480	protein F37B4.10 [518	32	40.5	768	2	T37601	penicillin-binding
446	32	40.5	331	2	S76480	hypothetical prote	519	32	40.5	781	2	T39373	probable transcript
447	32	40.5	341	2	C47083	hypothetical prote	520	32	40.5	788	2	C82595	dynamain-related pr
448	32	40.5	342	2	AH1045	conserved hypotet	521	32	40.5	826	2	C96694	ferric enterobacti
449	32	40.5	342	2	T26677	hypothetical prote	522	32	40.5	875	2	AB1125	hypothetical prote
450	32	40.5	348	2	AG1161	hypothetical prote	523	32	40.5	931	2	B75027	E. coli YbgG protei
451	32	40.5	351	2	S39603	class I histocompa	524	32	40.5	935	2	T51930	hypothetical prote
452	32	40.5	358	1	S74846	hypothetical prote	525	32	40.5	959	1	B71405	kinesin [imported]
453	32	40.5	375	1	A28630	muconate cyclisom	526	32	40.5	990	2	T12678	probable kinesin -
454	32	40.5	375	2	B64674	carbamoyl-phosphat	527	32	40.5	1000	1	A33620	hypothetical prote
455	32	40.5	375	2	T35015	probable 3-oxoadip	528	32	40.5	1000	1	C82630	myosin heavy chain
456	32	40.5	376	2	JC4892	L-selectin precurs	529	32	40.5	1011	2	S45573	serine proteinase
457	32	40.5	387	2	A47287	estradiol 17beta-d	530	32	40.5	1011	2	S45573	myosin IA - fruit
458	32	40.5	391	2	B97008	cyclopropane fatty	531	32	40.5	1013	2	T33470	hypothetical prote
459	32	40.5	401	2	T18661	hypothetical prote	532	32	40.5	1013	2	T33470	Ca2+-transporting
460	32	40.5	411	2	T17750	hypothetical prote	533	32	40.5	1025	2	T45811	kinesin-related pr
461	32	40.5	423	2	T48121	hypothetical prote	534	32	40.5	1066	1	A42640	kinesin-related pr
462	32	40.5	423	2	T51794	MYB DNA-binding-1	535	32	40.5	1111	1	A32684	myosin heavy chain
463	32	40.5	433	2	T47750	N2,N2-dimethylguan	536	32	40.5	1111	1	A48843	MHC class II trans
464	32	40.5	442	2	A35557	myosin heavy chain	537	32	40.5	1130	2	D98250	protein t21B10.3 [
465	32	40.5	463	2	G97300	aspartyl/asparagin	538	32	40.5	1132	2	D98250	endopeptidase La-1
466	32	40.5	464	2	T40108	glucan 1,3-beta-gl	539	32	40.5	1153	1	RWHU1B	cell surface glyco
467	32	40.5	466	2	B91186	probable permease	540	32	40.5	1170	2	T25043	hypothetical prote

541	32	40.5	1321	2	T13283	probable transcrip	614	31	39.2	211	2	C84751	hypothetical prote
542	32	40.5	1358	2	T29041	hypothetical prote	615	31	39.2	216	2	T26505	hypothetical prote
543	32	40.5	1389	2	T41230	hypothetical tpr d	616	31	39.2	221	2	S70755	conserved hypotet
544	32	40.5	1459	2	A12488	hypothetical prote	617	31	39.2	224	2	G89890	hypothetical prote
545	32	40.5	1532	2	T18438	hypothetical prote	618	31	39.2	224	2	T47397	hypothetical prote
546	32	40.5	1567	2	S11672	ice nucleation pro	619	31	39.2	227	2	S77870	dnak-type molecula
547	32	40.5	1784	2	T43167	sodium channel pro	620	31	39.2	230	2	C86141	protein T25K16.5 (
548	32	40.5	1937	2	I38055	myosin heavy chain	621	31	39.2	233	2	E89976	conserved hypotet
549	32	40.5	1938	1	A40997	myosin heavy chain	622	31	39.2	236	2	E89090	conserved hypotet
550	32	40.5	1938	1	S06005	myosin alpha heavy	623	31	39.2	236	2	T19789	hypothetical prote
551	32	40.5	1938	1	JK0178	myosin heavy chain	624	31	39.2	242	2	T48581	hypothetical prote
552	32	40.5	1938	2	A59293	skeletal myosin he	625	31	39.2	243	2	T28802	hypothetical prote
553	32	40.5	1938	2	I49464	alpha cardiac myos	626	31	39.2	249	2	S39698	nitro/flavin reduc
554	32	40.5	1939	1	A46762	myosin alpha heavy	627	31	39.2	256	2	B75079	hypothetical prote
555	32	40.5	1939	2	I48175	myosin heavy chain	628	31	39.2	262	2	A13518	nitrate reductase
556	32	40.5	1940	1	A24922	myosin heavy chain	629	31	39.2	263	2	AC0522	probable secreted
557	32	40.5	1940	1	S04090	myosin heavy chain	630	31	39.2	271	2	T47119	3-methyl-2-oxobuta
558	32	40.5	1940	2	A29320	myosin heavy chain	631	31	39.2	277	2	T05091	probable methyltra
559	32	40.5	1940	2	A59287	myosin heavy chain	632	31	39.2	280	2	AC3579	transcription regu
560	32	40.5	1974	2	T30010	hypothetical prote	633	31	39.2	284	1	S13676	deoxyribonuclease
561	32	40.5	1992	1	S02771	myosin heavy chain	634	31	39.2	295	2	T27475	hypothetical prote
562	32	40.5	2186	2	T13169	tiggrin - fruit fl	635	31	39.2	296	2	T06572	convicillin precurs
563	32	40.5	2332	1	GNV4F	genome polypeptide	636	31	39.2	301	2	S78543	drdp-4-dehydroxam
564	32	40.5	2539	2	B71619	hypothetical prote	637	31	39.2	301	2	S86486	protein P28J9.4 [1
565	32	40.5	2555	2	A40043	hypothetical prote	638	31	39.2	301	2	T51435	hypothetical prote
566	32	40.5	2592	2	T23768	notch protein homo	639	31	39.2	301	2	T01193	reverse transcript
567	32	40.5	6669	2	S55024	hypothetical prote	640	31	39.2	313	2	E83095	conserved hypotet
568	31.5	39.9	77	2	F95154	nebulin, skeletal	641	31	39.2	313	2	AE2812	conserved hypotet
569	31.5	39.9	346	2	D75303	hypothetical prote	642	31	39.2	315	2	A70313	NADH2 dehydrogenas
570	31.5	39.9	378	2	AE0484	conserved hypotet	643	31	39.2	322	2	H90057	conserved hypotet
571	31.5	39.9	379	2	S74601	probable glycerate	644	31	39.2	324	2	T18818	hypothetical prote
572	31.5	39.9	392	2	D64493	hypothetical prote	645	31	39.2	338	2	S75196	hypothetical prote
573	31.5	39.9	472	2	A33275	nonspecific lipid-	646	31	39.2	338	2	S56533	hypothetical prote
574	31.5	39.9	473	2	T19707	glycosomal protei	647	31	39.2	338	2	T43440	hypothetical 38K p
575	31.5	39.9	496	2	F83213	hypothetical prote	648	31	39.2	340	2	T27389	hypothetical prote
576	31.5	39.9	525	2	S48663	conserved hypotet	649	31	39.2	342	2	G96618	probable proline-r
577	31.5	39.9	540	1	S44830	phosphoenolpyruvat	650	31	39.2	343	2	A84335	chloromuconate cyc
578	31.5	39.9	788	1	I58282	F54F2.5 protein -	651	31	39.2	346	2	F97590	probable reductase
579	31	39.2	48	2	ABJ386	diacylglycerol kin	652	31	39.2	350	2	S44717	hypothetical prote
580	31	39.2	51	2	T41535	hypothetical prote	653	31	39.2	352	2	AH2039	hypothetical prote
581	31	39.2	58	1	WMTM68	60S ribosomal prot	654	31	39.2	354	2	S44724	outer membrane pro
582	31	39.2	63	2	T13265	6.8K ribosomal -	655	31	39.2	355	2	S47904	probable DOP zinc
583	31	39.2	90	2	S35438	Cro repressor prot	656	31	39.2	365	2	A98088	membrane-bound lyl
584	31	39.2	90	2	S62081	M-like protein pre	657	31	39.2	365	2	A65084	membrane-bound lyl
585	31	39.2	100	2	B40651	hypothetical prote	658	31	39.2	365	2	C85933	membrane-bound lyl
586	31	39.2	112	2	S51121	genome polypeptide	659	31	39.2	365	2	AD2811	conserved hypotet
587	31	39.2	116	2	C72731	hypothetical prote	660	31	39.2	368	2	C29356	hydroxyproline-ric
588	31	39.2	121	2	F69891	conserved hypotet	661	31	39.2	375	2	E70011	potassium channel
589	31	39.2	139	2	I40604	hypothetical prote	662	31	39.2	376	2	F81224	glycosyltransferas
590	31	39.2	142	2	C70059	hypothetical prote	663	31	39.2	377	2	A81996	glycosyltransferas
591	31	39.2	143	2	H83935	hypothetical prote	664	31	39.2	382	2	AH2056	hypothetical prote
592	31	39.2	144	2	T12102	glycine-rich prote	665	31	39.2	385	2	A40359	aliphatic amidase
593	31	39.2	145	2	F69214	heat shock protein	666	31	39.2	385	2	C83226	aliphatic amidase
594	31	39.2	152	2	D71569	probable hth trans	667	31	39.2	387	2	S61615	hypothetical prote
595	31	39.2	166	2	T25773	hypothetical prote	668	31	39.2	389	2	A55493	oxytocin receptor
596	31	39.2	173	2	T08011	2S seed storage pr	669	31	39.2	401	2	T42655	hypothetical prote
597	31	39.2	176	2	S52914	virion protein j13	670	31	39.2	405	2	A83781	transposase (01) B
598	31	39.2	181	2	S44765	C29E4.9 protein -	671	31	39.2	405	2	D83826	transposase (01) B
599	31	39.2	182	2	C90936	hypothetical prote	672	31	39.2	405	2	A84042	transposase (01) B
600	31	39.2	182	2	G85784	hypothetical prote	673	31	39.2	409	2	T06767	probable transcrip
601	31	39.2	182	2	A64935	hypothetical prote	674	31	39.2	409	2	T35598	hypothetical prote
602	31	39.2	183	2	S52904	virion protein j13	675	31	39.2	412	2	G69330	hypothetical prote
603	31	39.2	184	2	E72700	hypothetical prote	676	31	39.2	412	2	S48881	isocitrate dehydro
604	31	39.2	185	2	S52903	virion protein j13	677	31	39.2	415	2	S50963	rRNA (guanosine-2'
605	31	39.2	186	2	S28021	virion protein - Ar	678	31	39.2	415	2	B84858	hypothetical prote
606	31	39.2	189	2	S52902	virion protein j13	679	31	39.2	417	2	F96607	hypothetical prote
607	31	39.2	189	2	S52907	virion protein j13	680	31	39.2	417	2	E90844	probable clathrin-
608	31	39.2	189	2	S59399	hypothetical prote	681	31	39.2	417	2	H83708	hypothetical prote
609	31	39.2	191	2	S52905	virion protein j13	682	31	39.2	417	2	D85702	hypothetical prote
610	31	39.2	193	2	A82419	conserved hypotet	683	31	39.2	417	2	A64869	ychp protein - Bac
611	31	39.2	196	2	S52906	virion protein j13	684	31	39.2	422	2	A83184	probable protein m
612	31	39.2	208	2	G64416	hypothetical prote	685	31	39.2	422	2	T22732	hypothetical prote
613	31	39.2	210	2	D87394	hypothetical prote	686	31	39.2	425	2	H90415	hypothetical prote

687	31	39.2	428	1	I36930	involucrin - white	760	31	39.2	632	2	T18692	hypothetical prote
688	31	39.2	431	1	E70699	probable pkaA prot	761	31	39.2	635	2	C81861	hypothetical prote
689	31	39.2	440	2	C36014	Probable sugar upt	762	31	39.2	637	2	S74677	hypothetical prote
690	31	39.2	440	2	C34332	glutelin 3 precurs	763	31	39.2	649	2	F88651	protein B0212.1 [i
691	31	39.2	441	2	F83683	transposase (01) B	764	31	39.2	661	2	A55877	tumor necrosis fac
692	31	39.2	449	2	T51720	glucose-6-phosphat	765	31	39.2	663	2	S21912	BRcore-Q1-21 prote
693	31	39.2	455	2	C97256	uncharacterized pr	766	31	39.2	664	2	S02116	RNA helicase WSS11
694	31	39.2	457	2	C85434	glucosyltransferas	767	31	39.2	670	2	C83540	conserved hypothet
695	31	39.2	458	2	F97589	hypothetical prote	768	31	39.2	684	2	A97679	peptidyl-di-peptida
696	31	39.2	460	2	G90035	Tcaa protein [lmpo	769	31	39.2	686	2	AG2303	conserved hypothet
697	31	39.2	462	2	AF1945	PARA family protei	770	31	39.2	697	2	A86402	peptidyl-di-peptida
698	31	39.2	464	1	YKPG	semenogelin I prec	771	31	39.2	704	2	S21911	protein T22C5.17 [
699	31	39.2	464	1	YKPG	citrate (si)-synth	772	31	39.2	711	2	S73898	BRcore-NS-23 prote
700	31	39.2	468	2	JC5417	phosphoprotein pho	773	31	39.2	715	2	H84799	DNA topoisomerase
701	31	39.2	470	2	JN0431	RNA-directed RNA p	774	31	39.2	728	2	S21913	hypothetical prote
702	31	39.2	471	1	S08325	flavonol 3-O-glucu	775	31	39.2	732	1	HVHUK	BRcore-TN11-Q1-21
703	31	39.2	471	2	S01052	flavonol 3-O-glucu	776	31	39.2	741	2	F90739	Kell blood group p
704	31	39.2	471	2	S01037	flavonol 3-O-glucu	777	31	39.2	741	2	H85589	probable transport
705	31	39.2	472	2	A86347	branched-chain alp	778	31	39.2	762	2	E81371	probable transport
706	31	39.2	472	2	T51858	hypothetical prote	779	31	39.2	769	2	F89870	serine proteinase
707	31	39.2	472	2	T23534	melibiose carrier	780	31	39.2	772	2	T43034	kinesin-like prote
708	31	39.2	476	2	AC1023	ORD protein - frui	781	31	39.2	775	2	T43033	kinesin-like prote
709	31	39.2	476	2	S23576	glutelin 22 precu	782	31	39.2	786	2	H64817	probable membrane
710	31	39.2	479	2	S66578	glutelin - rice	783	31	39.2	794	2	T46242	similar to mammali
711	31	39.2	495	2	D34332	hypothetical prote	784	31	39.2	813	2	T46242	kinesin-like prote
712	31	39.2	496	2	S18745	NADPH-ferrihemopro	785	31	39.2	815	2	T41490	kinesin-like prote
713	31	39.2	498	2	S43776	Rieske [2Fe-2S] ir	786	31	39.2	823	2	T21943	hypothetical prote
714	31	39.2	506	2	S37156	permease of the Na	787	31	39.2	823	2	T21943	hypothetical prote
715	31	39.2	508	2	G84133	BRcore-Z protein -	788	31	39.2	830	2	AX0528	myosin s-1 heavy c
716	31	39.2	513	2	F96943	spindle pole body-	789	31	39.2	862	2	A05028	rpoC protein homol
717	31	39.2	514	2	S21914	hypothetical prote	790	31	39.2	880	2	F84029	valyl-tRNA synthet
718	31	39.2	517	2	A57280	hypothetical prote	791	31	39.2	881	2	E82097	protein-P-II uridy
719	31	39.2	517	2	T02464	butyrophilin precu	792	31	39.2	887	2	S43196	[protein-PiI] urid
720	31	39.2	526	2	S70587	butyrophilin - bov	793	31	39.2	890	2	AX0528	[protein-PiI] urid
721	31	39.2	526	2	T37821	chromosomal replic	794	31	39.2	890	2	G64740	protein PII-uridyl
722	31	39.2	527	2	AI3494	gene ND5 intron 1	795	31	39.2	890	2	A85501	protein PII-uridyl
723	31	39.2	533	2	S10841	homeotic protein b	796	31	39.2	890	2	A90650	probable proline-r
724	31	39.2	538	1	S12570	zinc finger 2 prote	797	31	39.2	890	2	G84693	probable DNA repai
725	31	39.2	540	2	S57785	ND5 intron 2 prote	798	31	39.2	897	2	T37813	hypothetical prote
726	31	39.2	544	2	S09143	glutamate-tRNA lig	799	31	39.2	906	2	AG1957	hypothetical prote
727	31	39.2	552	2	S65787	glutamate-tRNA lig	800	31	39.2	906	2	AG1957	[protein-PiI] urid
728	31	39.2	553	2	B69167	probable AMP-bindi	801	31	39.2	912	2	AI0127	hemoglobin-binding
729	31	39.2	555	2	A83327	hypothetical prote	802	31	39.2	953	2	B64083	probable membrane
730	31	39.2	555	2	T26413	hypothetical prote	803	31	39.2	1009	2	S20538	chitin synthase (E
731	31	39.2	559	2	C83250	30S ribosomal prot	804	31	39.2	1021	2	T15765	chitin synthase (E
732	31	39.2	561	2	G81842	30S ribosomal prot	805	31	39.2	1026	2	T18220	probable maturase
733	31	39.2	561	2	G81099	hypothetical prote	806	31	39.2	1035	2	S78159	probable complemen
734	31	39.2	567	2	T16105	acetate-CoA ligase	807	31	39.2	1053	2	S46139	probable polyprote
735	31	39.2	567	2	AF3611	hypothetical prote	808	31	39.2	1054	2	G85079	hemoglobin-binding
736	31	39.2	569	2	T17779	hypothetical prote	809	31	39.2	1084	2	B64088	hypothetical prote
737	31	39.2	571	2	S00566	convicilin precurs	810	31	39.2	1110	2	T29327	hypothetical prote
738	31	39.2	580	2	AG1342	mannose-6-phosphat	811	31	39.2	1113	2	T47381	probable polyprote
739	31	39.2	582	2	T16104	hypothetical prote	812	31	39.2	1138	2	G85077	probable DNA-direc
740	31	39.2	586	1	RNEGB1	DNA-directed RNA p	813	31	39.2	1144	2	A81983	DNA polymerase III
741	31	39.2	586	2	T02978	asparagine synthas	814	31	39.2	1144	2	H81037	tumor suppressor p
742	31	39.2	594	2	S72638	hypothetical ABC e	815	31	39.2	1162	2	F90247	reverse gyrase (co
743	31	39.2	598	1	RDEBFV	fumarate reductase	816	31	39.2	1166	2	T03814	metabotropic gluta
744	31	39.2	598	2	AG0311	NADH2 dehydrogenas	817	31	39.2	1171	2	A42916	metabotropic gluta
745	31	39.2	600	1	D65000	NADH2 dehydrogenas	818	31	39.2	1171	2	T42372	metabotropic gluta
746	31	39.2	600	2	AD0797	NADH dehydrogenase	819	31	39.2	1189	1	JC21132	protein-tyrosine-p
747	31	39.2	600	2	C85869	NADH dehydrogenase	820	31	39.2	1180	2	JC21132	protein-tyrosine-p
748	31	39.2	600	2	B91025	ribophorin I precu	821	31	39.2	1187	1	UC4155	probable chromosom
749	31	39.2	605	2	A27274	hypothetical prote	822	31	39.2	1194	2	T37503	hypothetical prote
750	31	39.2	605	2	T04197	hypothetical prote	823	31	39.2	1198	2	B86402	hypothetical prote
751	31	39.2	605	2	T26088	terminal protein p	824	31	39.2	1201	2	F86386	metabotropic gluta
752	31	39.2	606	1	UZAD12	ribophorin I precu	825	31	39.2	1215	2	JC2131	probable retroelem
753	31	39.2	607	2	A26168	hemagglutinin - ri	826	31	39.2	1256	2	F88886	brain-specific ang
754	31	39.2	609	1	HMN2KA	hemagglutinin - ri	827	31	39.2	1262	2	F88886	protein P52G2.2 [i
755	31	39.2	609	2	S43009	probable ATP-depen	828	31	39.2	1273	1	TDRTLT	leukocyte common a
756	31	39.2	613	2	F64056	hypothetical prote	829	31	39.2	1305	2	H96559	hypothetical prote
757	31	39.2	615	2	B86713	ABC transporter, A	830	31	39.2	1312	2	D85066	hypothetical prote
758	31	39.2	619	2	F82391	DNA mismatch repai	831	31	39.2				
759	31	39.2	623	2	AI3637		832	31	39.2				

833	31	39.2	1314	2	T47331	hypothetical prote	906	30	38.0	149	2	F72153	P4R protein - vari
834	31	39.2	1388	2	T47961	hypothetical prote	907	30	38.0	149	2	D16839	C4R protein - vari
835	31	39.2	1472	2	A84470	hypothetical prote	908	30	38.0	150	2	S50063	probable endonucle
836	31	39.2	1485	1	IS2PT2	DNA topoisomerase	909	30	38.0	151	2	D86638	conserved hypothet
837	31	39.2	1643	2	T07961	myosin heavy chain	910	30	38.0	154	2	S55630	hypothetical prote
838	31	39.2	1648	2	S57163	probable membrane	911	30	38.0	154	2	I47153	transcription fact
839	31	39.2	1756	2	T02599	hypothetical prote	912	30	38.0	157	2	B46243	epidermal growth f
840	31	39.2	1767	2	T00458	hypothetical prote	913	30	38.0	161	2	A00836	probable bacteriop
841	31	39.2	1770	2	S69953	hypothetical prote	914	30	38.0	161	2	AD0930	probable phase tai
842	31	39.2	1887	2	C86478	Tyb protein - yeas	915	30	38.0	161	2	AG1034	probable phage tai
843	31	39.2	1911	2	T43048	protein F1504.13 [916	30	38.0	161	2	D86418	unknown protein, 6
844	31	39.2	1970	2	T03284	calcium channel al	917	30	38.0	162	2	H83459	Cytochrome C-type
845	31	39.2	2121	2	A59233	myoblast city prot	918	30	38.0	167	2	A37246	myelin basic prote
846	31	39.2	2248	2	A35938	profilaggrin - hum	919	30	38.0	175	2	T50968	hypothetical prote
847	31	39.2	3924	2	S37431	ankyrin 2, neuroa	920	30	38.0	176	2	S50822	b2P protein - whe
848	30.5	38.6	174	2	D86852	hypothetical prote	921	30	38.0	179	2	G44477	hypothetical prote
849	30.5	38.6	193	2	S16399	papJ protein precu	922	30	38.0	179	2	AH2835	soluble lytic tran
850	30.5	38.6	264	1	E70027	probable 3-oxoacyl	923	30	38.0	185	2	AF2073	hypothetical prote
851	30.5	38.6	299	2	T12483	hypothetical prote	924	30	38.0	186	2	T47428	hypothetical prote
852	30.5	38.6	392	1	A37157	3-methyl-2-oxobuta	925	30	38.0	188	2	F69262	hypothetical prote
853	30.5	38.6	412	2	T34415	hypothetical prote	926	30	38.0	192	2	G89756	cellulium resistan
854	30.5	38.6	596	2	B87112	conserved hypothet	927	30	38.0	195	2	C97613	probable transglyc
855	30.5	38.6	755	2	A12174	penicillin-binding	928	30	38.0	197	2	AE2120	Cytochrome c oxida
856	30.5	38.6	995	2	T05842	hypothetical prote	929	30	38.0	197	2	I50469	RAG-1 protein - sa
857	30.5	38.6	1039	2	T22982	hypothetical prote	930	30	38.0	198	2	A70013	sulfite oxidase ho
858	30.5	38.6	1180	2	T20773	hypothetical prote	931	30	38.0	200	2	A44762	outer membrane pro
859	30.5	38.6	1192	2	H86293	protein F59B10.1 [932	30	38.0	202	1	A44247	C4b-binding protei
860	30.5	38.6	1525	1	GNWY55	genome polyprotein	933	30	38.0	203	2	AG2120	hypothetical prote
861	30.5	38.6	4549	2	T20771	hypothetical prote	934	30	38.0	207	2	T08109	oleosin-like prote
862	30.5	38.6	4667	2	T20774	hypothetical prote	935	30	38.0	207	2	H86429	hypothetical prote
863	30	38.0	20	2	S68617	histone H2A - sea	936	30	38.0	212	2	H75277	hypothetical prote
864	30	38.0	49	2	T07307	hypothetical prote	937	30	38.0	213	2	A21177	Ig light chain pre
865	30	38.0	55	2	B70120	hypothetical prote	938	30	38.0	215	2	H87602	flagellin modifca
866	30	38.0	62	2	A34326	protamine - chicke	939	30	38.0	216	2	T10254	S11 protein, self-
867	30	38.0	63	2	D95169	hypothetical prote	940	30	38.0	220	2	T28639	y4JL protein - Rhi
868	30	38.0	65	1	GACH	protamine - chicke	941	30	38.0	222	2	AE1164	transglycosylase h
869	30	38.0	66	2	H95110	ribosomal protein	942	30	38.0	223	2	S44974	lmbu protein - Str
870	30	38.0	66	2	F97979	50S ribosomal prot	943	30	38.0	223	2	AE1523	replication initia
871	30	38.0	67	2	T44077	hypothetical prote	944	30	38.0	229	1	Q0SAEC	phosphoglycolate p
872	30	38.0	71	2	D82155	hypothetical prote	945	30	38.0	231	2	B49934	exotoxin 11 [impor
873	30	38.0	76	2	B72173	H11R protein - var	946	30	38.0	231	2	D89807	protein F13A2.8 [i
874	30	38.0	81	2	D82631	hypothetical prote	947	30	38.0	232	2	G89025	hypothetical prote
875	30	38.0	86	2	T28871	hypothetical prote	948	30	38.0	233	2	F64482	transcription regu
876	30	38.0	90	1	DNECS2	DNA-binding protei	949	30	38.0	233	2	AF3522	maturational-associ
877	30	38.0	90	2	AH0931	histone like DNA-b	950	30	38.0	243	2	S27758	hypothetical prote
878	30	38.0	90	2	C91244	DNA-binding protei	951	30	38.0	243	2	G86701	3-oxoacyl-(acyl-ca
879	30	38.0	90	2	A86092	DNA-binding protei	952	30	38.0	245	2	AE3517	S11 protein - Chac
880	30	38.0	90	2	A31388	DNA-binding protei	953	30	38.0	245	2	S43774	glycerol uptake fa
881	30	38.0	91	2	AC0454	DNA-binding protei	954	30	38.0	245	2	D86780	heme exporter prot
882	30	38.0	94	2	A84966	integration host f	955	30	38.0	245	2	H91014	heme exporter prot
883	30	38.0	100	2	AD1410	cellobiose phospho	956	30	38.0	245	2	B85859	heme exporter prot
884	30	38.0	102	2	AC1786	cellobiose phospho	957	30	38.0	245	2	E64989	heme exporter prot
885	30	38.0	102	2	S73743	hypothetical prote	958	30	38.0	250	2	T16631	NADPH-flavin oxido
886	30	38.0	103	2	B26167	Ig lambda chain C	959	30	38.0	251	2	A84019	hypothetical prote
887	30	38.0	106	2	I50584	RAG-1 protein - nu	960	30	38.0	251	2	S75353	hypothetical prote
888	30	38.0	107	2	D83918	hypothetical prote	961	30	38.0	253	2	T33533	hypothetical prote
889	30	38.0	108	2	AH0176	probable sulfite r	962	30	38.0	256	2	D69789	hypothetical prote
890	30	38.0	117	2	S01822	Ig heavy chain V-D	963	30	38.0	256	2	T48588	hypothetical prote
891	30	38.0	117	2	E71899	hypothetical prote	964	30	38.0	257	2	AE3190	3-oxoacyl-(acyl-ca
892	30	38.0	119	2	A69881	conserved hypothet	965	30	38.0	259	2	S56646	chaperonin 60 beta
893	30	38.0	119	2	AC2351	hypothetical prote	966	30	38.0	260	2	C36827	protein F20B17.2 [
894	30	38.0	123	2	A97138	uncharacterized pr	967	30	38.0	263	2	A81197	DNA repair protein
895	30	38.0	124	2	T39810	hypothetical prote	968	30	38.0	263	2	G83738	transcription regu
896	30	38.0	125	1	HSUR9M	histone H2A, gonad	969	30	38.0	264	2	A81834	DNA repair protein
897	30	38.0	132	2	H59093	hypothetical prote	970	30	38.0	266	2	I49050	Ly-49E-GE antigen
898	30	38.0	132	2	T46905	hypothetical prote	971	30	38.0	266	2	I49051	Ly-49F-GE antigen
899	30	38.0	137	2	S68956	nucleoside-diphosp	972	30	38.0	274	2	T05769	myb-related protei
900	30	38.0	138	2	AH0100	hypothetical prote	973	30	38.0	278	2	B69663	formamidopyrimidin
901	30	38.0	141	2	H64909	yfdo protein - Esc	974	30	38.0	278	2	T39517	dual-specificity M
902	30	38.0	147	2	A53180	ribonuclease PL3 (975	30	38.0	280	2	A98934	hypothetical prote
903	30	38.0	147	2	C64223	hypothetical prote	976	30	38.0	280	2	E85782	hypothetical prote
904	30	38.0	149	1	WMVZK7	K7 protein 28R - v	977	30	38.0	280	2	S10873	regulatory protein
905	30	38.0	149	2	T28462	hypothetical prote	978	30	38.0	282	1	NHU1	deoxyribonuclease

979 30 38.0 284 2 T23636
980 30 38.0 285 2 C64750
981 30 38.0 286 2 S67183
982 30 38.0 287 2 F81705
983 30 38.0 289 2 C87899
984 30 38.0 291 1 A31305
985 30 38.0 291 1 S18718
986 30 38.0 293 2 H70366
987 30 38.0 297 2 A72100
988 30 38.0 297 2 A86524
989 30 38.0 297 2 B95200
990 30 38.0 297 2 A98067
991 30 38.0 299 2 C35213
992 30 38.0 299 2 G64969
993 30 38.0 300 2 S76144
994 30 38.0 301 2 E72384
995 30 38.0 302 2 C49906
996 30 38.0 302 2 D81692
997 30 38.0 302 2 T24091
998 30 38.0 302 2 A69749
999 30 38.0 303 2 H86245
1000 30 38.0 306 2 H75358

hypothetical prote
probable transcrip
hypothetical prote
conserved hypothe
protein F16C3.2 [i
transcription fact
transcription fact
lysyl-tRNA synthet
4-hydroxybenzoate
benzoate octapheny
ABC transporter, A
hypothetical prote
rfbc protein - Shi
dUDP-4-dehydroram
hypothetical prote
ABC transporter, A
rfbc homolog - Xan
conserved hypothe
hypothetical prote
bifunctional nucle
LAO/AO transport s

ALIGNMENTS

RESULT 1
S28261
centromere protein E - human
N/Alternate names: centromere 312K protein; kinesin-related protein CENP-E
C/Species: Homo sapiens (man)
C/Date: 03-Mar-1994 #sequence_revision 03-Mar-1994 #text_change 09-Jul-2004
C/Accession: S28261
R/Yen, T.J.; Li, G.; Schaar, B.T.; Szilak, I.; Cleveland, D.W.
Nature 359, 536-539, 1992
A/Title: CENP-E is a putative kinetochore motor that accumulates just before mitosis.
A/Reference number: S28261; PMID:93024922; PMID:1406971
A/Accession: S28261
A/Molecule type: mRNA
A/Residues: 1-2663 <YEN>
A/Cross-references: UNIPROT:Q02224; UNIPARC:UPI00001274FC; EMBL:Z15005; NID:g29864; PIDN
C/Genetics:
A/Gene: GDB:CENPE
A/Cross-references: GDB:361164; OMIM:117143
A/Map position: 4q24-q25
C/Superfamily: centromere protein E; kinesin motor domain homology
C/Keywords: ATP; coiled coil; microtubule binding; mitosis; nucleotide binding; P-loop
F/7-335/Domain: kinesin motor domain homology <KMT>
F/86-93/Region: nucleotide-binding motif A (P-loop)
F/486-2183/Domain: coiled coil #status predicted <COI>
F/92/Binding site: ATP (Lys) #status predicted

Query Match 100.0%; Score 79; DB 1; Length 2663;
Best Local Similarity 100.0%; Pred. No. 9.8e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RHYGETKMNQSSRS 15
DB 189 RHYGETKMNQSSRS 203

RESULT 2
T14156
kinesin-related protein - African clawed frog
C/Species: Xenopus laevis (African clawed frog)
C/Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 09-Jul-2004
C/Accession: T14156
R/Wood, K.W.; Sakowicz, R.; Goldstein, L.S.; Cleveland, D.W.
Cell 91, 357-366, 1997
A/Title: CENP-E is a plus end-directed kinetochore motor required for metaphase chromos
A/Reference number: T17893; PMID:96028574; PMID:9363944
A/Accession: T14156

103 A:Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: mRNA
A/Residues: 1-2954 <WOO>
A/Cross-references: UNIPROT:O42263; UNIPARC:UPI00000FDD80; EMBL:AF027728; NID:g2586070;
C/Genetics:
A/Gene: XCENP-E
C/Superfamily: centromere protein E; kinesin motor domain homology

Query Match 87.3%; Score 69; DB 2; Length 2954;
Best Local Similarity 86.7%; Pred. No. 0.00074;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 RHYGETKMNQSSRS 15
DB 187 RHYGETKMNQSSRS 201

RESULT 3
T52425
kinesin-like protein [imported] - Arabidopsis thaliana
C/Species: Arabidopsis thaliana (mouse-ear cress)
C/Date: 24-Oct-2000 #sequence_revision 24-Oct-2000 #text_change 09-Jul-2004
C/Accession: T52425
R/Kato, A.; Suzuki, M.; Kuwahara, A.; Ooe, H.; Higano-Inaba, K.; Komeda, Y.
Gene 239, 309-316, 1999
A/Title: Isolation and analysis of cDNA within a 300 kb Arabidopsis thaliana genomic reg
A/Reference number: Z25171
A/Accession: T52425
A:Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: mRNA
A/Residues: 1-823 <KAT>
A/Cross-references: UNIPROT:Q9S7P3; UNIPARC:UPI000009F1FC; EMBL:AB028468; PIDN:BAA88112.
C/Genetics:
A/Gene: ZCF125

Query Match 73.4%; Score 58; DB 2; Length 823;
Best Local Similarity 73.3%; Pred. No. 0.021; 3; Indels 0; Gaps 0;
Matches 11; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 RHYGETKMNQSSRS 15
DB 184 RHYGETKMNQSSRS 198

RESULT 4
D96619
protein T30E16.9 [imported] - Arabidopsis thaliana
C/Species: Arabidopsis thaliana (mouse-ear cress)
C/Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004
C/Accession: D96619
R/Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso,
Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.,
ansen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000
A/Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.
C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali,
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A/Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon,
ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A/Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A/Reference number: A86141; PMID:21016719; PMID:11130712
A/Accession: D96619
A:Status: preliminary
A:Molecule type: DNA
A/Residues: 1-888 <STO>
A/Cross-references: UNIPROT:Q9LQ62; UNIPARC:UPI00000A1D8E; GB:AE005173; NID:g8778739; PI
C/Genetics:
A/Gene: T30E16.9
A/Map position: 1

Query Match 73.4%; Score 58; DB 2; Length 888;
Best Local Similarity 73.3%; Pred. No. 0.023;
Matches 11; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 RHYGETKNQSRSS 15
 ||:|||||
 Db 215 RHFGTNNVHSSRS 229
 ||:|||||

RESULT 5
 A47334
 Lckin kinesin-related antigen - Leishmania chagasi (fragment)
 C:Species: Leishmania chagasi
 C>Date: 21-Sep-1993 #sequence_revision 18-Nov-1994 #text_change 31-Dec-2004
 C:Accession: A47334
 R:Burns Jr., J.M.; Shreffler, W.G.; Benson, D.R.; Ghalib, H.W.; Badato, R.; Reed, S.G.
 Proc. Natl. Acad. Sci. U.S.A. 90, 775-779, 1993
 A:Title: Molecular characterization of a kinesin-related antigen of Leishmania chagasi
 A:Reference number: A47334; MUID:93133867; PMID:8421715
 A:Accession: A47334
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-955 <BUR>
 A:Cross-references: UNIPROT:P46865; UNIPARC:UPI000012DE6D; GB:L07879; NID:G308884; PIDN:
 A:Experimental source: MHOM/BR/82/BA-2.C1
 A:Note: sequence extracted from NCBI backbone (NCBIN:122864, NCBIP:122865)
 A:Keywords: ATP; nucleotide binding; P-loop
 F:13-398/Domain: kinesin motor domain homology <KMOT>
 F:122-129/Region: nucleotide-binding motif A (P-loop)

Query Match 68.4%; Score 54; DB 2; Length 955;
 Best Local Similarity 73.3%; Pred. No. 0.13;
 Matches 11; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 RHYGETKNQSRSS 15
 ||:|||||
 Db 241 RHTASTKNDRSSRS 255
 ||:|||||

RESULT 6
 F84599
 probable kinesin heavy chain [imported] - Arabidopsis thaliana
 C:Species: Arabidopsis thaliana (mouse-ear cress)
 C>Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 09-Jul-2004
 C:Accession: F84599
 R:Lin, X.; Kaul, S.; Rounlev, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;
 M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L.;
 euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter,
 Nature 402, 761-768, 1999
 A:Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
 A:Reference number: A84420; MUID:20083487; PMID:10617197
 A:Accession: F84599
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-581 <STO>
 A:Cross-references: UNIPROT:Q9SJU7; UNIPARC:UPI000009D929; GB:AE002093; NID:G4567265; PI
 A:Gene: At2g21300
 A:Map position: 2

Query Match 64.6%; Score 51; DB 2; Length 581;
 Best Local Similarity 66.7%; Pred. No. 0.28;
 Matches 10; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 RHYGETKNQSRSS 15
 ||:|||||
 Db 205 RKIGETSLNRSRS 219
 ||:|||||

RESULT 7
 T06055
 hypothetical protein F19H22.50 - Arabidopsis thaliana
 C:Species: Arabidopsis thaliana (mouse-ear cress)
 C>Date: 30-Apr-1999 #sequence_revision 30-Apr-1999 #text_change 09-Jul-2004
 C:Accession: T06055
 R:Bevan, M.; Murphy, G.; Ridley, P.; Hudson, S.; Hudson, S.; Bancroft, I.; Mewes, H.W.; Mayer, K.F.X

submitted to the Protein Sequence Database, March 1999
 A:Reference number: Z15184
 A:Accession: T06055
 A:Molecule type: DNA
 A:Residues: 1-834 <BEV>
 A:Cross-references: UNIPROT:Q9SVJ8; UNIPARC:UPI000009EC9D; EMBL:AL035679; GSPDB:GN00062;
 A:Experimental source: cultivar Columbia; BAC clone F19H22
 C:Genetics:
 A:Gene: AtSP:F19H22.50
 A:Map position: 4
 A:Introns: 63/1; 93/1; 126/3; 164/3; 196/2; 234/3; 276/2; 389/3; 422/3; 633/3; 726/2
 C:Superfamily: kinesin heavy chain; kinesin motor domain homology
 F:14-339/Domain: kinesin motor domain homology <KMOT>

Query Match 64.6%; Score 51; DB 2; Length 834;
 Best Local Similarity 66.7%; Pred. No. 0.41;
 Matches 10; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 RHYGETKNQSRSS 15
 ||:|||||
 Db 214 RKIGETSLNRSRS 228
 ||:|||||

RESULT 8
 T30196
 kinesin motor protein 1 - smut fungus (Ustilago maydis)
 C:Species: Ustilago maydis (corn smut)
 C>Date: 22-Oct-1999 #sequence_revision 22-Oct-1999 #text_change 09-Jul-2004
 C:Accession: T30196
 R:Lehmle, C.; Steinberg, G.; Snetelaar, K.M.; Schliwa, M.; Kahmann, R.; Bolker, M.
 EMBO J. 16, 3464-3473, 1997
 A:Title: Identification of a motor protein required for filamentous growth in Ustilago m
 A:Reference number: Z20770; MUID:97361828; PMID:9218789
 A:Accession: T30196
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-1459 <LEH>
 A:Cross-references: UNIPROT:P87198; UNIPARC:UPI000006C405; EMBL:U92844; NID:G2062749; PI
 C:Genetics:
 A:Gene: kin1
 C:Function:
 A:Description: required for filamentous growth in Ustilago maydis

Query Match 63.3%; Score 50; DB 2; Length 1459;
 Best Local Similarity 66.7%; Pred. No. 1.1;
 Matches 10; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 RHYGETKNQSRSS 15
 ||:|||||
 Db 487 RHVGATDWNRSRS 501
 ||:|||||

RESULT 9
 E86183
 hypothetical protein [imported] - Arabidopsis thaliana
 C:Species: Arabidopsis thaliana (mouse-ear cress)
 C>Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004
 C:Accession: E86183
 R:Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso,
 Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.;
 ansen, N.F.; Hughes, B.; Huizar, L.
 Nature 408, 816-820, 2000
 A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.
 C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziani,
 Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
 A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon,
 ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
 A:Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
 A:Reference number: A86141; MUID:21016719; PMID:11130712
 A:Accession: E86183
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-198 <STO>

F:397-739/Domain: kinesin motor domain homology <KMOT>
F:481-488/Region: nucleotide-binding motif A (P-loop)

Query Match 59.5%; Score 47; DB 2; Length 754;

Best Local Similarity 60.0%; Pred. No. 2;
Matches 9; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 1 RHYGETKNQRRSRS 15

Db 598 RSVGKTQMQEQRSS 612

RESULT 15

S34830
kinesin-related protein ktaA - Arabidopsis thaliana
N:Alternate names: protein F7J7.210; protein T6K22.10
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 09-Dec-1993 #sequence revision 01-Dec-1995 #text_change 05-Oct-2004
C:Accession: S34830; T04958; T05170

R:Mitui, H.; Yamaguchi-Shinozaki, K.; Shinozaki, K.; Nishikawa, K.; Takahashi, H.

Mol. Gen. Genet. 238, 362-368, 1993

A:Title: Identification of a gene family (kat) encoding kinesin-like proteins in Arabid

A:Reference number: S34830; MUID:93261419; PMID:8492804

A:Accession: S34830

A:Molecule type: mRNA

A:Residues: 1-793 <MIT>

A:CROSS-references: UNIPROT:Q07970; UNIPARC:UPI000012DC4E; EMBL:D11371; NID:g303501; PID

R:Bevan, M.; Murphy, G.; Ridley, P.; Hudson, S.; Bancroft, I.; Mewes, H.W.; Mayer, K.P.X

submitted to the Protein Sequence Database, July 1998

A:Reference number: Z15391

A:Accession: T04958

A:Molecule type: DNA

A:Residues: 1-793 <BEV>

A:CROSS-references: UNIPARC:UPI000012DC4E; EMBL:AL021960

A:Experimental source: cultivar Columbia; BAC clone F7J7

R:Bevan, M.; Peters, S.A.; van Staveren, M.; Dirks, W.; Stiekema, W.; Bancroft, I.; Mew

submitted to the Protein Sequence Database, August 1998

A:Reference number: Z15400

A:Accession: T05170

A:Molecule type: DNA

A:Residues: 1-397 <BEV>

A:CROSS-references: UNIPARC:UPI0000000354; EMBL:AL031187

A:Experimental source: cultivar Columbia; BAC clone T6K22

C:Genetics:

A:Gene: ktaA

A:Map position: 4

A:Introns: 15/3; 89/3; 138/1; 174/3; 214/3; 282/3; 352/3; 377/3; 426/3; 473/1; 509/3; 56

A:Note: F7J7.210; T6K22.10

C:Keywords: ATP; nucleotide binding; P-loop

F:432-778/Domain: Kinesin motor domain homology <KMOT>

F:516-523/Region: nucleotide-binding motif A (P-loop)

Query Match 59.5%; Score 47; DB 2; Length 793;

Best Local Similarity 60.0%; Pred. No. 2,1;

Matches 9; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 1 RHYGETKNQRRSRS 15

Db 637 RSVGKTQMQEQRSS 651

RESULT 16

E85814

hypothetical protein Z3056 [imported] - Escherichia coli (strain O157:H7, substrain EDL9

C:Species: Escherichia coli

C:Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 09-Jul-2004

C:Accession: E85814

R:Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew

iller, L.; Grobeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apodaca,

Nature 409, 529-533, 2001

A:Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.

A:Reference number: A85480; MUID:21074935; PMID:11206551

A:Accession: E85814

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-102 <STO>

A:CROSS-references: UNIPROT:Q8XB88; UNIPARC:UPI0000165823; GB:AE005174; NID:g12516072; F

A:Experimental source: strain O157:H7, substrain EDL933

C:Genetics:

A:Gene: Z3056

C:Superfamily: Escherichia coli probable membrane protein b1963

Query Match 58.2%; Score 46; DB 2; Length 102;

Best Local Similarity 69.2%; Pred. No. 0.4;

Matches 9; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 3 YGETKNQRRSRS 15

Db 24 YGSTMEEELRSRS 36

RESULT 17

E90966

hypothetical protein ECs2701 [imported] - Escherichia coli (strain O157:H7, substrain RI

C:Species: Escherichia coli

C:Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 09-Jul-2004

C:Accession: E90966

R:Hayaashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Lehi, K.; Yokoyama, K.; Han, C.G.

gasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.

Gen. Res. 8, 11-22, 2001

A:Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and ganc

A:Reference number: A99629; MUID:21156231; PMID:11258796

A:Accession: E90966

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-108 <HAY>

A:CROSS-references: UNIPROT:Q8XB88; UNIPARC:UPI0000D060B; GB:BA000007; PIDN:BA036124.1;

A:Experimental source: strain O157:H7, substrain RMD 0509952

C:Genetics:

A:Gene: ECs2701

C:Superfamily: Escherichia coli probable membrane protein b1963

Query Match 58.2%; Score 46; DB 2; Length 108;

Best Local Similarity 69.2%; Pred. No. 0.42;

Matches 9; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 3 YGETKNQRRSRS 15

Db 30 YGSTMEEELRSRS 42

RESULT 18

G64960

probable membrane protein b1963 - Escherichia coli (strain K-12)

C:Species: Escherichia coli

C:Date: 12-Sep-1997 #sequence_revision 17-Sep-1997 #text_change 01-Mar-2002

C:Accession: G64960

R:Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; Co

.A.; Rose, D.J.; Mau, B.; Shao, Y.

Science 277, 1453-1462, 1997

A:Title: The complete genome sequence of Escherichia coli K-12.

A:Reference number: A64720; MUID:97426617; PMID:9278503

A:Accession: G64960

A:Status: nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA

A:Residues: 1-127 <BLAT>

A:CROSS-references: UNIPARC:UPI00001680F0; GB:AE000288; GB:U00096; NID:g2367124; PIDN:A

A:Experimental source: strain K-12, substrain MG1655

C:Superfamily: Escherichia coli probable membrane protein b1963

C:Keywords: transmembrane protein

F:93-109/Domain: transmembrane #status predicted <TW1>

Query Match 58.2%; Score 46; DB 2; Length 127;

Best Local Similarity 69.2%; Pred. No. 0.5;

Matches 9; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

```
QY      3 YGETKNQRRSSRS 15
      |||||:|||||
Db      30 YGSTWMEERLSRS 42
      |||||:|||||

RESULT 19
T49235
kinesin-like protein - Arabidopsis thaliana
N:Alternate names: protein F7K15.60
C:Species: Arabidopsis thaliana (mouse-ear cress)
C>Date: 02-Jun-2000 #sequence_revision 02-Jun-2000 #text_change 09-Jul-2004
C:Accession: T49235
R:Obermaier, B.; Ottenwaelder, B.; Duchemin, D.; Zeitler, K.; Mewes, H.W.; Rudd, S.; Lem
submitted to the Protein Sequence Database, April 2000
A:Reference number: Z25019
A:Accession: T49235
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-932 <OBE>
A:Cross-references: UNIPROT:Q9LXL3; UNIPARC:UPI0000052DA8; EMBL:AL353871; GSPDB:GN000061;
A:Experimental source: cultivar Columbia; BAC clone F7K15
C:Genetics:
A:Gene: ATSP:F7K15.60
A:Map position: 3
A:Introns: 76/1; 106/1; 139/3; 177/3; 205/1; 227/3; 247/3; 289/2; 355/3; 401/3; 430/3; 7

Query Match      58.2%; Score 46; DB 2; Length 932;
Best Local Similarity 60.0%; Pred. No. 3.8;
Matches 9; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY      1 RHYGETKNQRRSSRS 15
      |||||:|||||
Db      207 RQVGETALNDKSSRS 221

RESULT 20
C44259
kinesin heavy chain homolog KIF5 - mouse (fragment)
C:Species: Mus musculus (house mouse)
C>Date: 10-Jun-1993 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004
C:Accession: C44259
R:Aizawa, H.; Sekine, Y.; Takemura, R.; Zhang, Z.; Nangaku, M.; Hirokawa, N.
J. Cell Biol. 119, 1287-1296, 1992
A:Title: Kinesin family in murine central nervous system.
A:Reference number: A44259; MUID:93077686; PMID:1447303
A:Accession: C44259
A>Status: preliminary; not compared with conceptual translation
A:Molecule type: nucleic acid
A:Residues: 1-143 <AI2>
A:Cross-references: UNIPROT:P33175; UNIPARC:UPI00001775C7
A:Experimental source: brain
A>Note: sequence extracted from NCBI backbone (NCBIP:118906)
C:Superfamily: kinesin motor domain; kinesin motor domain homology
F:1-143/Domain: kinesin motor domain homology (fragment) <KNOT>

Query Match      57.0%; Score 45; DB 2; Length 143;
Best Local Similarity 60.0%; Pred. No. 0.86;
Matches 9; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY      1 RHYGETKNQRRSSRS 15
      |||||:|||||
Db      103 RHVAVTNMNESSRS 117

RESULT 21
AF1393
glycosyl transferases homolog lmo2550 [imported] - Listeria monocytogenes (strain EGD-e)
C:Species: Listeria monocytogenes
C>Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 09-Jul-2004
C:Accession: AF1393
R:Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloecker,
.; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsihi, H.
.; Jones, L.M.; Karst, U.
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Science 294, 849-852, 2001
A:Authors: Krefte, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; Ma
ok, C.; Schluster, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehländ,
A:Title: Comparative Genomics of Listeria species.
A:Reference number: AB1077; MUID:21537279; PMID:11679669
A:Accession: AF1393
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-315 <GLA>
A:Cross-references: UNIPROT:Q93RNO; UNIPARC:UPI0000054EBA; GB:NC_003210; PIDN:CAD00628.1
A:Experimental source: strain EGD-e
C:Genetics:
A:Gene: lmo2550
C:Superfamily: stress response protein csbB

Query Match      57.0%; Score 45; DB 2; Length 315;
Best Local Similarity 75.0%; Pred. No. 1.9;
Matches 9; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      1 RHYGETKNQRRS 12
      |||||:|||||
Db      201 RHAGETKNYRS 212

RESULT 22
A11768
glycosyl transferases homolog lin2695 [imported] - Listeria innocua (strain Cliph11262)
C:Species: Listeria innocua
C>Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 09-Jul-2004
C:Accession: A11768
R:Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloecker,
.; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsihi, H.
.; Jones, L.M.; Karst, U.
Science 294, 849-852, 2001
A:Authors: Krefte, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; Ma
ok, C.; Schluster, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehländ,
A:Title: Comparative genomics of Listeria species.
A:Reference number: AB1077; MUID:21537279; PMID:11679669
A:Accession: A11768
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-315 <GLA>
A:Cross-references: UNIPROT:Q927U3; UNIPARC:UPI00000CC955; GB:AL592022; PIDN:CAC97921.1;
A:Experimental source: strain Cliph11262
C:Genetics:
A:Gene: lin2695
C:Superfamily: stress response protein csbB

Query Match      57.0%; Score 45; DB 2; Length 315;
Best Local Similarity 75.0%; Pred. No. 1.9;
Matches 9; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      1 RHYGETKNQRRS 12
      |||||:|||||
Db      201 RHAGETKNYRS 212

RESULT 23
C85065
kinesin-like protein [imported] - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C>Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 09-Jul-2004
C:Accession: C85065
R:anonymous, The European Union Arabidopsis Genome Sequencing Consortium, The Cold Sprin
Nature 402, 769-777, 1999
A:Title: Sequence and analysis of chromosome 4 of the plant Arabidopsis thaliana.
A:Reference number: AB5001; MUID:20083488; PMID:10617198
A:Accession: C85065
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-777 <STO>
A:Cross-references: UNIPROT:Q9M0X6; UNIPARC:UPI00000A7F28; GB:NC_001268; NID:g7262729; P
C:Genetics:
```

A:Gene: AT4g05190
A:Map position: 4
C:Superfamily: kinesin-related protein KLRPA; kinesin motor domain homology

Query Match 57.0%; Score 45; DB 2; Length 777;
Best Local Similarity 60.0%; Pred. No. 4.8;
Matches 9; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1 RHYGETKNQSRSS 15
|||:|:|:|:|
DB 621 RSVGKTHMNEQSSRS 635

RESULT 24
A41919
kinesin heavy chain - human
N:Contains: kinesin ATPase (EC 3.6.1.-)
C:Species: Homo sapiens (man)
C:Date: 03-Mar-1994 #sequence_revision 03-Mar-1994 #text_change 09-Jul-2004
C:Accession: A41919; S24603
R:Navone, F.; Niclas, J.; Hom-Booher, N.; Sparks, L.; Bernstein, H.D.; McCaffrey, G.; Va
J. Cell Biol. 117, 1263-1275, 1992
A:Title: Cloning and expression of a human kinesin heavy chain gene: interaction of the
A:Reference number: A41919; MUID:92299683; PMID:1607388
A:Accession: A41919
A:Status: nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 1-963 <NAV>
A:Cross-references: UNIPROT:P33176; UNIPARC:UPI000012DE68; GB:X65873; NID:g34082; PIDN:C
C:Genetics:
A:Gene: GDB:KNS1; KNS
A:Cross-references: GDB:13532
C:Superfamily: kinesin heavy chain; kinesin motor domain homology
C:Keywords: ATP; coiled coil; heterotetramer; hydrolase; microtubule binding; nucleotide
F:9-331/Domain: kinesin motor domain homology <KMOT>
F:85-92/Region: nucleotide-binding motif A (P-loop)
F:402-860/Domain: rod #status predicted <RDD>
F:861-963/Domain: globular #status predicted <GBD>
F:91/Binding site: ATP (Lys) #status predicted

Query Match 57.0%; Score 45; DB 1; Length 963;
Best Local Similarity 60.0%; Pred. No. 6;
Matches 9; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 1 RHYGETKNQSRSS 15
|||:|:|:|:|
DB 190 RHVAVTNMNEHSSRS 204

RESULT 25
A35075
kinesin heavy chain - longfin squid
N:Contains: kinesin ATPase (EC 3.6.1.-)
C:Species: Loligo pealeii (longfin squid)
C:Date: 03-Mar-1994 #sequence_revision 03-Mar-1994 #text_change 09-Jul-2004
C:Accession: A35075
R:Kosik, K.S.; Orecchio, L.D.; Schnapp, B.; Inouye, H.; Neve, R.L.
J. Biol. Chem. 265, 3278-3283, 1990
A:Title: The primary structure and analysis of the squid kinesin heavy chain.
A:Reference number: A35075; MUID:90153980; PMID:2137456
A:Accession: A35075
A:Molecule type: mRNA
A:Residues: 1-967 <KOS>
A:Cross-references: UNIPROT:P21613; UNIPARC:UPI000012DE69; GB:J05258; NID:g460682; PIDN:
C:Superfamily: kinesin heavy chain; kinesin motor domain homology
C:Keywords: ATP; coiled coil; heterotetramer; hydrolase; methylated amino acid; microtub
F:9-332/Domain: kinesin motor domain homology <KMOT>
F:85-92/Region: nucleotide-binding motif A (P-loop)
F:392-861/Domain: rod #status predicted <RDD>
F:862-967/Domain: globular #status predicted <GBD>
F:27-174, 206/Binding site: phosphate (Ser) (covalent) #status predicted
F:32/Modified site: N6,N6-trimethyllysine (Lys) #status predicted
F:91/Binding site: ATP (Lys) #status predicted

F:546/Binding site: phosphate (Thr) (covalent) #status predicted

Query Match 57.0%; Score 45; DB 1; Length 967;
Best Local Similarity 60.0%; Pred. No. 6;
Matches 9; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 1 RHYGETKNQSRSS 15
|||:|:|:|:|
DB 190 RHVAVTNMNEHSSRS 204

RESULT 26
A31497
kinesin heavy chain - fruit fly (Drosophila melanogaster)
N:Contains: kinesin ATPase (EC 3.6.1.-)
C:Species: Drosophila melanogaster
C:Date: 03-Mar-1994 #sequence_revision 03-Mar-1994 #text_change 09-Jul-2004
C:Accession: A31497
R:Yang, J.T.; Laymon, R.A.; Goldstein, L.S.B.
Cell 56, 879-889, 1989
A:Title: A three-domain structure of kinesin heavy chain revealed by DNA sequence and m
A:Reference number: A31497; MUID:89168428; PMID:2522352
A:Accession: A31497
A:Molecule type: mRNA
A:Residues: 1-975 <YAN>
A:Cross-references: UNIPROT:P17210; UNIPARC:UPI000011EE2A; GB:M24441; NID:gl57777; PIDN:
C:Genetics:
A:Gene: FlyBase:Khc
A:Cross-references: FlyBase:FBgn0001308
C:Superfamily: kinesin heavy chain; kinesin motor domain homology
C:Keywords: ATP; coiled coil; heterotetramer; hydrolase; microtubule binding; nucleotide
F:13-339/Domain: kinesin motor domain homology <KMOT>
F:92-99/Region: nucleotide-binding motif A (P-loop)
F:399-883/Domain: rod #status predicted <RDD>
F:884-975/Domain: globular #status predicted <GBD>
F:98/Binding site: ATP (Lys) #status predicted

Query Match 57.0%; Score 45; DB 1; Length 975;
Best Local Similarity 60.0%; Pred. No. 6;
Matches 9; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 1 RHYGETKNQSRSS 15
|||:|:|:|:|
DB 197 RHVAVTNMNEHSSRS 211

RESULT 27
S37711
kinesin heavy chain - mouse
C:Species: Mus musculus (house mouse)
C:Date: 09-Dec-1993 #sequence_revision 26-May-1995 #text_change 09-Jul-2004
C:Accession: S37711
R:Kato, K.
J. Neurosci. 2, 704-711, 1991
A:Title: A collection of cDNA clones with specific expression patterns in mouse brain.
A:Reference number: S37707
A:Accession: S37711
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: mRNA
A:Residues: 1-1027 <KAT>
A:Cross-references: UNIPROT:P28738; UNIPARC:UPI000016CE7C; EMBL:X61435; NID:g52796; PIDN:
C:Superfamily: kinesin heavy chain; kinesin motor domain homology
C:Keywords: nucleotide binding; P-loop
F:9-333/Domain: kinesin motor domain homology <KMOT>
F:86-93/Region: nucleotide-binding motif A (P-loop)

Query Match 57.0%; Score 45; DB 2; Length 1027;
Best Local Similarity 60.0%; Pred. No. 6.4;
Matches 9; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 1 RHYGETKNQSRSS 15
|||:|:|:|:|

Db 191 RHVAVTNMNEHSRS 205

RESULT 28

A38713

Kinesin heavy chain - sea urchin (Strongylocentrotus purpuratus)

N:Contains: kinesin ATPase (SC 3.6.1.-)

C:Species: Strongylocentrotus purpuratus (purple urchin)

C>Date: 03-Mar-1994 #sequence_revision 03-Mar-1994 #text_change 09-Jul-2004

C:Accession: A38713; S24308

R:Wright, B.D.; Henson, J.H.; Wedaman, K.P.; Willy, P.J.; Morand, J.N.; Scholey, J.M.

J. Cell Biol. 113, 817-833, 1991

A:Title: Subcellular localization and sequence of sea urchin kinesin heavy chain: evidence from cDNA and complementary DNA

A:Reference number: A38713; MUID:91225077; PMID:1827446

A:Accession: A38713

A:Molecule type: mRNA

A:Residues: 1-1031 <WRI>

A:Cross-references: UNIPROT:P35978; UNIPARC:UPI000012DE6B; GB:X56844; NID:gl0269; PIDN:C42640

C:Superfamily: kinesin heavy chain; kinesin motor domain homology

C:Keywords: ATP; coiled coil; heterotetramer; hydrolase; microtubule binding; mitosis; n

F:9-331/Domain: kinesin motor domain homology <KMOT>

F:84-91/Region: nucleotide-binding motif A (P-loop)

F:393-857/Domain: rod #status predicted <RDD>

F:858-1031/Domain: globular #status predicted <GSD>

F:90/Binding site: ATP (Lys) #status predicted

Query Match 57.0%; Score 45; DB 1; Length 1031;

Best Local Similarity 60.0%; Pred. No. 6.4;

Matches 9; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

Qy 1 RHYGETKNQSSRS 15

Db 189 RHVAVTNMNEHSRS 203

RESULT 29

I38510

neuronal kinesin heavy chain - human

C:Species: Homo sapiens (man)

C>Date: 29-May-1998 #sequence_revision 29-May-1998 #text_change 09-Jul-2004

C:Accession: I38510

R:Niclas, J.; Navone, F.; Hom-Booher, N.; Vale, R.D.

Neuron 12, 1059-1072, 1994

A:Title: Cloning and localization of a conventional kinesin motor expressed exclusively from cerebellar granule cells

A:Reference number: I38510; MUID:94242426; PMID:7514426

A:Accession: I38510

A>Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-1032 <RES>

A:Cross-references: UNIPROT:Q12840; UNIPARC:UPI000012DE6E; EMBL:U06698; NID:g497123; PIDN:U06698

C:Superfamily: kinesin heavy chain; kinesin motor domain homology

C:Keywords: nucleotide binding; P-loop

F:10-333/Domain: kinesin motor domain homology <KMOT>

F:86-93/Region: nucleotide-binding motif A (P-loop)

Query Match 57.0%; Score 45; DB 2; Length 1032;

Best Local Similarity 60.0%; Pred. No. 6.4;

Matches 9; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

Qy 1 RHYGETKNQSSRS 15

Db 191 RHVAVTNMNEHSRS 205

RESULT 30

S38983

Kinesin-related protein 95K chain - sea urchin (Strongylocentrotus purpuratus) (fragment)

C:Species: Strongylocentrotus purpuratus (purple urchin)

C>Date: 07-Oct-1994 #sequence_revision 07-Feb-1997 #text_change 02-Feb-2001

C:Accession: S38983; S72552

R:Coile, D.G.; Chinn, S.W.; Wedaman, K.P.; Hall, K.; Vuong, T.; Scholey, J.M.

Nature 366, 268-270, 1993

A:Title: Novel heterotrimeric kinesin-related protein purified from sea urchin eggs.

A:Reference number: S38982; MUID:94050179; PMID:8232586

A:Accession: S38983

A>Status: nucleic acid sequence not shown

A:Molecule type: mRNA

A:Residues: 1-294 <COL1>

A:Cross-references: UNIPARC:UPI00001775CA; GB:U00996

A:Accession: S72552

A:Molecule type: protein

A:Residues: 247-264 <COL2>

A:Cross-references: UNIPARC:UPI00001775CB

C:Superfamily: kinesin-related protein KIF3; kinesin motor domain homology

C:Keywords: nucleotide binding; P-loop

F:1-279/Domain: kinesin motor domain homology (fragment) <KMOT>

F:29-36/Region: nucleotide-binding motif A (P-loop)

Query Match 55.7%; Score 44; DB 2; Length 294;

Best Local Similarity 60.0%; Pred. No. 2.7;

Matches 9; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

Qy 1 RHYGETKNQSSRS 15

Db 134 RSVGSTNMNEHSRS 148

RESULT 31

C42640

kinesin-related protein KIP2 - yeast (Saccharomyces cerevisiae)

A:Alternate names: protein P2581; protein YPL155c

C:Species: Saccharomyces cerevisiae

C>Date: 03-Mar-1994 #sequence_revision 03-Mar-1994 #text_change 09-Jul-2004

C:Accession: C42640; S65166; S69444; S28232; S28234

R:Roof, D.M.; Meluh, P.B.; Rose, M.D.

J. Cell Biol. 118, 95-108, 1992

A:Title: Kinesin-related proteins required for assembly of the mitotic spindle.

A:Reference number: A42640; MUID:92317166; PMID:1618910

A:Accession: C42640

A:Molecule type: DNA

A:Residues: 1-706 <ROO>

A:Cross-references: UNIPROT:P28743; UNIPARC:UPI000012DE72; EMBL:Z11963; NID:g3852; PIDN:U000012DE72

A>Note: sequence extracted from NCBI backbone (NCBI:107719, NCBIP:107722)

R:Purnelle, B.; Coster, F.; Goffeau, A.

submitted to the Protein Sequence Database, May 1996

A:Reference number: S65154

A:Accession: S65154

A:Molecule type: DNA

A:Residues: 1-706 <PUR>

A:Cross-references: UNIPARC:UPI000012DE72; EMBL:Z73511; NID:gl370329; PIDN:CAA97860.1; P

A:Experimental source: strain S288C (AB972)

R:Purnelle, B.; Combiez, S.; Coster, F.; Naveau, F.; Goffeau, A.

submitted to the EMBL Data Library, March 1996

A:Description: The sequence of 55 kb on the left arm of yeast chromosome XVI identifies a gene to the human phosphotyrosyl phosphatase activator PTPA and a homologue to the plant

A:Reference number: S69428

A:Accession: S69444

A:Molecule type: DNA

A:Residues: 1-706 <PUN>

A:Cross-references: UNIPARC:UPI000012DE72; EMBL:X96770; NID:gl403537; PIDN:CAA65566.1; P

C:Genetics:

A:Gene: SGD.KIP2; MIPS.YPL155c

A:Cross-references: SGD.S0006076; MIPS.YPL155c

A:Map position: 16L

C:Superfamily: kinesin-related protein KIF2; kinesin motor domain homology

C:Keywords: ATP; coiled coil; microtubule binding; nucleotide binding; P-loop

F:159-499/Domain: kinesin motor domain homology #status atypical <KMOT>

F:202-209/Region: nucleotide-binding motif A (P-loop)

F:208/Binding site: ATP (Lys) #status predicted

Query Match 55.7%; Score 44; DB 1; Length 706;

Best Local Similarity 66.7%; Pred. No. 6.6;

Matches 10; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 1 RHYGETKNQSSRS 15

Db 330 RKIGETDYNARSSRS 344

RESULT 32

S58691

Kinesin-related protein KRP95 - sea urchin (Strongylocentrotus droebachiensis)

N:Alternate names: kinesin-2 chain B; KRP (85/95) 95K chain

C:Species: Strongylocentrotus droebachiensis

C>Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004

C:Accession: S58691

J. Rashid, D.J.; Wedaman, K.P.; Scholey, J.M.

J. Mol. Biol. 252, 157-162, 1995

A:Title: Heterodimerization of the two motor subunits of the heterotrimeric kinesin, KRP

A:Reference number: S58691; MUID:95404610; PMID:7674298

A:Accession: S58691

A>Status: preliminary; nucleic acid sequence not shown; not compared with conceptual tra

A:Molecule type: mRNA

A:Residues: 1-742 <RAS>

A:Cross-references: UNIPROT:O7M453; UNIPARC:UPI0000173E01

C:Complex: heterotrimer of a 115K chain and two kinesin-related chains of 85K (PIR:S3898

C:Superfamily: kinesin-related protein KIF3; kinesin motor domain homology

C:Keywords: ATP; heterotrimer; microtubule binding; nucleotide binding; P-loop

F:9-345/Domain: kinesin motor domain homology <KMOT>

F:95-102/Region: nucleotide-binding motif A (P-loop)

F:101/Binding site: ATP (Lys) #status predicted

Query Match 55.7%; Score 44; DB 1; Length 742;

Best Local Similarity 60.0%; Pred. No. 7;

Matches 9; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 1 RHYGETKNQRSSRS 15

DB 200 RSVGSTNNNEHSSRS 214

RESULT 33

B56766

protein kinesin F2P9.27 [imported] - Arabidopsis thaliana

C:Species: Arabidopsis thaliana (mouse-ear cress)

C>Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004

C:Accession: B96766

R:Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso,

ansen, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.;

Nature 408, 816-820, 2000

C:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.

C:Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Lueros, J.S.; Maiti, R.; Marziali,

Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.

A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon,

ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.

A:Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.

A:Reference number: A86141; MUID:21016719; PMID:11130712

A:Accession: B96766

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-987 <STO>

A:Cross-references: UNIPROT:Q9C9A8; UNIPARC:UPI00000A435A; GB:AE005173; NID:g7109485; PI

C:Genetics:

A:Gene: F2P9.27

A:Map position: 1

Query Match 55.7%; Score 44; DB 2; Length 987;

Best Local Similarity 60.0%; Pred. No. 9.3;

Matches 9; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 RHYGETKNQRSSRS 15

DB 698 RAVGSTALNERSRS 712

RESULT 34

T21134

hypothetical protein F20C5.2 - Caenorhabditis elegans

C:Species: Caenorhabditis elegans

C>Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004

C:Accession: T21134

R:Matthews, P.

submitted to the EMBL Data Library, December 1995

A:Reference number: Z19381

A:Accession: T21134

A>Status: preliminary; translated from GB/EMBL/DDBJ

A:Molecule type: DNA

A:Residues: 1-1130 <WIL>

A:Cross-references: UNIPROT:Q8MQ68; UNIPARC:UPI0000079539; EMBL:Z68161; PIDN:CAA92295.1;

A:Experimental source: clone F20C5

C:Genetics:

A:Gene: CESP:F20C5.2

A:Map position: 4

A:Introns: 15/3; 34/2; 69/2; 152/3; 183/3; 207/2; 314/3; 513/3; 546/2; 594/1; 632/3; 667

Query Match 55.7%; Score 44; DB 2; Length 1130;

Best Local Similarity 60.0%; Pred. No. 11;

Matches 9; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 1 RHYGETKNQRSSRS 15

DB 204 RSVGRTNNNEHSSRS 218

RESULT 35

C48835

kinesin-like protein (clone XKlp3) Klp - African clawed frog (fragment)

C:Species: Xenopus laevis (African clawed frog)

C>Date: 01-Dec-1993 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004

C:Accession: C48835

R:Vernos, I.; Headman, J.; Wylie, C.

Dev. Biol. 157, 232-239, 1993

A:Title: Multiple kinesin-like transcripts in Xenopus oocytes.

A:Reference number: A48835; MUID:93246065; PMID:8482413

A:Accession: C48835

A>Status: preliminary; not compared with conceptual translation

A:Molecule type: mRNA

A:Residues: 1-332 <VER>

A:Cross-references: UNIPROT:Q93478; UNIPARC:UPI00001775C9

A:Experimental source: oocytes

A>Note: sequence extracted from NCBI backbone (NCBI:P130977)

C:Superfamily: kinesin-related protein KIF3; kinesin motor domain homology

C:Keywords: nucleotide binding; P-loop

F:1-332/Domain: kinesin motor domain homology (fragment) <KMOT>

F:87-94/Region: nucleotide-binding motif A (P-loop)

Query Match 54.4%; Score 43; DB 2; Length 332;

Best Local Similarity 60.0%; Pred. No. 4.7;

Matches 9; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 1 RHYGETKNQRSSRS 15

DB 192 RSVGATNNNEHSSRS 206

RESULT 36

B44259

kinesin-related protein KIF3A - mouse

C:Species: Mus musculus (house mouse)

C>Date: 03-Mar-1994 #sequence_revision 03-Mar-1994 #text_change 09-Jul-2004

C:Accession: B44259; S27872

J:Aizawa, H.; Sekine, Y.; Takemura, R.; Zhang, Z.; Nangaku, M.; Hirokawa, N.

J. Cell Biol. 119, 1287-1296, 1992

A:Title: Kinesin family in murine central nervous system.

A:Reference number: A44259; MUID:93077686; PMID:1447303

A:Accession: B44259

A:Molecule type: mRNA

A:Residues: 1-701 <AIIZ>

A:Cross-references: UNIPROT:P28741; UNIPARC:UPI0000028DDC; EMBL:D12645; NID:g230469; PID

A:Experimental source: brain

A>Note: sequence extracted from NCBI backbone (NCBI:P118911)

C;Complex: heterodimer with KIF3B (PIR:AS7107); the KIF3A/3B heterodimer associates with C;Function:
A;Description: KIF3 complex is a motor protein that provides anterograde fast axonal tra
C;Superfamily: kinesin-related protein KIF3; kinesin motor domain homology
C;Keywords: ATP; coiled coil; heterodimer; heterotrimer; microtubule binding; nucleotide
F;1-368/Domain: head globular #status predicted <HGL>
F;15-351/Domain: kinesin motor domain homology <KMOT>
F;100-107/Region: nucleotide-binding motif A (p-loop)
F;369-599/Domain: helical rod #status predicted <ROD>
F;600-701/Domain: tail globular #status predicted <TGL>
F;106/Binding site: ATP (Lys) #status predicted

Query Match 54.4%; Score 43; DB 1; Length 701;
Best Local Similarity 60.0%; Pred. No. 10;
Matches 9; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 1 RHYGETKNQSRSSRS 15
| | | | |
Db 206 RSVGATNNHSSRS 220
| | | | |

RESULT 37
AS7107
kinesin-related protein KIF3B - mouse
C;Species: Mus musculus (house mouse)
C;Date: 03-Nov-1995 #sequence_revision 03-Nov-1995 #text_change 09-Jul-2004
C;Accession: AS7107
R;Yamazaki, H.; Nakata, T.; Okada, Y.; Hirokawa, N.
J. Cell Biol. 130, 1387-1399, 1995
A;Title: KIF3A/3B, a heterodimeric kinesin superfamily protein that works as a microtubul
A;Reference number: AS7107; MUID:96032268; PMID:7559760
A;Accession: AS7107
A;Status: nucleic acid sequence not shown
A;Molecule type: mRNA
A;Residues: 1-747 <YAM>
A;Cross-references: UNIPROT:Q61771; UNIPARC:UPI000028ED1; GB:D26077; NID:G1060922; PIDN
A;Experimental source: brain
C;Complex: heterodimer with KIF3A (PIR:B44259); the KIF3A/3B heterodimer associates with
C;Function:
A;Description: KIF3 complex is a motor protein that provides anterograde fast axonal tra
C;Superfamily: kinesin-related protein KIF3; kinesin motor domain homology
C;Keywords: ATP; coiled coil; heterodimer; heterotrimer; microtubule binding; nucleotide
F;1-363/Domain: head globular #status predicted <HGL>
F;10-346/Domain: kinesin motor domain homology <KMOT>
F;96-103/Region: nucleotide-binding motif A (p-loop)
F;364-592/Domain: helical rod #status predicted <ROD>
F;594-747/Domain: tail globular #status predicted <TGL>
F;102/Binding site: ATP (Lys) #status predicted

Query Match 54.4%; Score 43; DB 1; Length 747;
Best Local Similarity 60.0%; Pred. No. 11;
Matches 9; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 1 RHYGETKNQSRSSRS 15
| | | | |
Db 201 RSVGATNNHSSRS 215
| | | | |

RESULT 38
AS3939
kinesin homolog KHP1 - Chlamydomonas reinhardtii
C;Species: Chlamydomonas reinhardtii
C;Date: 07-Oct-1994 #sequence_revision 07-Oct-1994 #text_change 31-Dec-2004
C;Accession: AS3939
R;Walther, Z.; Vashishtha, M.; Hall, J.L.
J. Cell Biol. 126, 175-188, 1994
A;Title: The Chlamydomonas FLA10 gene encodes a novel kinesin-homologous protein.
A;Reference number: AS3939; MUID:94299638; PMID:8027176
A;Accession: AS3939
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-786 <WAL>
A;Cross-references: UNIPROT: P46869; UNIPARC:UPI000012A838; EMBL:L33697; NID:G497696; PID

A;Note: authors translated the codon AAC for residue 753 as Asp
C;Genetics:
A;Gene: FLA10
C;Keywords: ATP; coiled coil; nucleotide binding; P-loop
F;11-359/Domain: kinesin motor domain homology <KMOT>
F;97-104/Region: nucleotide-binding motif A (P-loop)

Query Match 54.4%; Score 43; DB 2; Length 786;
Best Local Similarity 66.7%; Pred. No. 11;
Matches 10; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 RHYGETKNQSRSSRS 15
| | | | |
Db 203 RQVGATLMNQDSRS 217
| | | | |

RESULT 39
T45746
hypothetical protein F24M12.190 - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 04-Feb-2000 #sequence_revision 04-Feb-2000 #text_change 09-Jul-2004
C;Accession: T45746
R;Vitale, D.; Liguori, R.; Flores, M.; Argiriou, A.; De Simone, V.; Mewes, H.W.; Lemcke,
submitted to the Protein Sequence Database, December 1999
A;Reference number: Z23012
A;Accession: T45746
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-968 <VIT>
A;Cross-references: UNIPROT:Q9SD31; UNIPARC:UPI00000AB745; EMBL:AL132980
A;Experimental source: cultivar Columbia; HAC clone F24M12
C;Genetics:
A;Map position: 3
A;Introns: 69/1; 99/1; 132/3; 170/3; 198/1; 220/3; 242/3; 284/2; 396/3; 441/3; 514/1; 81
A;Note: F24M12.190

Query Match 54.4%; Score 43; DB 2; Length 968;
Best Local Similarity 60.0%; Pred. No. 14;
Matches 9; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 RHYGETKNQSRSSRS 15
| | | | |
Db 200 RQIGETALNEVSSRS 214
| | | | |

RESULT 40
C96661
kinesin-like protein, 73641-79546 [imported] - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004
C;Accession: C96661
R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federpiel, N.A.; Kaul, S.; White, O.; Alonso,
Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Dewar, K.;
ansen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000
A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.
C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali,
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon,
ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A;Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A;Reference number: A86141; MUID:21016719; PMID:11130712
A;Accession: C96661
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-1056 <STO>
A;Cross-references: UNIPROT:Q9CAC9; UNIPARC:UPI00000A6962; GB:AE005173; NID:G6456171; P11
C;Genetics:
A;Gene: F24D7.17
A;Map position: 1

Query Match 54.4%; Score 43; DB 2; Length 1056;
Best Local Similarity 60.0%; Pred. No. 15;

N:Alternate names: kinesin-like protein, KAR3-related, KLPA protein
C:Species: *Emmericella nidulans*, *Aspergillus nidulans*
C:Date: 03-Mar-1994 #sequence_revision 03-Mar-1994 #text_change 09-Jul-2004
C:Accession: A44337; S24830
R:O'Connell, M.J.; Meluh, P.B.; Rose, M.D.; Morris, N.R.
J. Cell Biol. 120, 153-162, 1993
A:Title: Suppression of the bimC4 mitotic spindle defect by deletion of klpA, a gene encoding a kinesin-like protein.
A:Reference number: A44337; MUID:93107178; PMID:8416986
A:Accession: A44337
A:Molecule type: mRNA
A:Residues: 1-770 <OLC>
A:Cross-references: UNIPROT:P28739; UNIPARC:UPI000012DER6; GB:X64603; NID:g2703; PIDN:CA
A>Note: sequence extracted from NCBI backbone (NCBIP:121121)
C:Genetics:
A:Gene: KlpA
A:Map position: 1
C:Superfamily: kinesin-related protein KLPA; kinesin motor domain homology
C:Keywords: ATP; coiled coil; microtubule binding; nucleotide binding; P-loop
F:422-762/Domain: kinesin motor domain homology <XMOT>
F:514-521/Region: nucleotide-binding motif A (P-loop)
F:520/Binding site: ATP (Lys) #status predicted

Query Match 51.9%; Score 41; DB 1; Length 770;
Best Local Similarity 60.0%; Pred. No. 26;
Matches 9; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 1 RHYGETKMNQSSRS 15
Db 619 RSVATKANERSRS 633
|||:|||||

RESULT 46
T38749
kinesin-like protein 1 - fission yeast (*Schizosaccharomyces pombe*)
N:Contains: adenosinetriphosphatase (EC 3.6.1.3)
C:Species: *Schizosaccharomyces pombe*
C:Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
C:Accession: T38749; T48658; T11636
R:Olliver, K.; Harris, D.; Wood, V.; Barrell, B.G.; Rajandream, M.A.
submitted to the EMBL Data Library, September 1996
A:Reference number: Z1809
A:Accession: T38749
A:Status: preliminary; translated from GB/EMBL/DBDJ
A:Molecule type: DNA
A:Residues: 1-832 <OLI>
A:Cross-references: UNIPROT:Q92376; UNIPARC:UPI000012DEF0; EMBL:Z59236; PIDN:CAB16597.1;
A:Experimental source: strain 972h-; cosmid c3H5
R:Pidoux, A.L.; Ledizet, M.; Cande, W.Z.
Mol. Biol. Cell 7, 1639-1655, 1996
A:Title: Fission yeast is a kinesin-related protein involved in mitotic spindle function
A:Reference number: Z24510; MUID:97053988; PMID:8898367
A:Accession: T48658
A:Status: preliminary; translated from GB/EMBL/DBDJ
A:Molecule type: mRNA
A:Residues: 1-342, 'D', 344-832 <PID>
A:Cross-references: UNIPARC:UPI00001691C6; EMBL:U63916; PIDN:AAB88235.1
A:Experimental source: strain 972h(-)
R:Barrell, B.G.; Rajandream, M.A.; Wood, V.
submitted to the EMBL Data Library, September 1997
A:Reference number: Z17303
A:Accession: T11636
A:Status: preliminary; translated from GB/EMBL/DBDJ
A:Molecule type: DNA
A:Residues: 761-832 <BAR>
A:Cross-references: UNIPARC:UPI000169036; EMBL:Z99260; NID:e1061997; PID:e349380
C:Genetics:
A:Gene: SPDB:SPAC3H5.03c
A:Map position: 1
A:Introns: 4/3; 216/1; 778/3
A>Note: SPAC3A11.14c
A>Note: intron positions not resolved (incomplete sequence)
C:Function:
A:Description: pkl1 shows microtubule-stimulated ATPase activity, nucleotide-sensitive B

C:Superfamily: kinesin-related protein KLPA; kinesin motor domain homology
C:Keywords: hydrolase; microtubule binding

Query Match 51.9%; Score 41; DB 2; Length 832;
Best Local Similarity 60.0%; Pred. No. 28;
Matches 9; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 1 RHYGETKMNQSSRS 15
Db 680 RFAATKANERSRS 694
|||:|||||

RESULT 47
T03792
kinesin-related protein tck1 - common tobacco
C:Species: *Nicotiana tabacum* (common tobacco)
C:Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 09-Jul-2004
C:Accession: T03792
R:Wang, W.; Takezawa, D.; Narasimulu, S.B.; Reddy, A.S.N.; Poovaiah, B.W.
Plant Mol. Biol. 31, 87-100, 1996
A:Title: A novel kinesin-like protein with a calmodulin-binding domain.
A:Reference number: Z15089; MUID:96309387; PMID:8704162
A:Accession: T03792
A:Status: preliminary; translated from GB/EMBL/DBDJ
A:Molecule type: mRNA
A:Residues: 1-1265 <WAN>
A:Cross-references: UNIPROT:O24147; UNIPARC:UPI00000AD012; EMBL:U52078; NID:g1491930; PI
A:Experimental source: cultivar Petit Havana SR-1; tissue-type anthers
C:Genetics:
A:Gene: tck1
F:890-1221/Domain: kinesin motor domain homology <XMOT>

Query Match 51.9%; Score 41; DB 2; Length 1265;
Best Local Similarity 60.0%; Pred. No. 42;
Matches 9; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 RHYGETKMNQSSRS 15
Db 1075 RHTTGTLNQEQRSS 1089
|||:|||||

RESULT 48
T07397
kinesin heavy chain-like protein (clone PKCBP) - potato
C:Species: *Solanum tuberosum* (potato)
C:Date: 14-May-1999 #sequence_revision 14-May-1999 #text_change 09-Jul-2004
C:Accession: T07397
R:Reddy, A.S.; Narasimulu, S.B.; Safadi, F.; Golovkin, M.
Plant J. 10, 9-21, 1996
A:Title: A plant kinesin heavy chain-like protein is a calmodulin-binding protein.
A:Reference number: Z16008; MUID:96314858; PMID:8758976
A:Accession: T07397
A:Status: preliminary; translated from GB/EMBL/DBDJ
A:Molecule type: mRNA
A:Residues: 1-1265 <RED>
A:Cross-references: UNIPROT:Q41460; UNIPARC:UPI00000AAB8C; EMBL:L46702; NID:g1369851; PI
C:Keywords: GTP binding; microtubule binding
F:890-1216/Domain: kinesin motor domain homology <XMOT>

Query Match 51.9%; Score 41; DB 2; Length 1265;
Best Local Similarity 60.0%; Pred. No. 42;
Matches 9; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 RHYGETKMNQSSRS 15
Db 1075 RHTTGTLNQEQRSS 1089
|||:|||||

RESULT 49
D85058
hypochemical protein AT4g04630 [imported] - *Arabidopsis thaliana*
C:Species: *Arabidopsis thaliana* (mouse-ear cress)
C:Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 09-Jul-2004

C:Accession: D85058
 R:Anonymous, The European Union Arabidopsis Genome Sequencing Consortium, The Cold Spring
 Nature 402, 769-777, 1999
 A:Title: Sequence and analysis of chromosome 4 of the plant Arabidopsis thaliana.
 A:Reference number: A85001; MUID:20083488; PMID:10617198

A:Accession: D85058
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-202 <STO>
 A:Cross-references: UNIPROT:Q9XEB6; UNIPARC:UPI00000A86FC; GB:NC_001268; NID:g7267221; F
 C:Genetics:
 A:Gene: AT4G04630
 A:Map position: 4

Query Match 50.6%; Score 40; DB 2; Length 202;
 Best Local Similarity 53.6%; Pred. NO. 10;
 Matches 7; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 3 YGETKMNQRS 13
 ||:| |:
 DB 91 YGDSKSNRRSS 101

RESULT 50

A75088
 hypothetical protein PAB1640 - Pyrococcus abyssi (strain Orsay)
 C:Species: Pyrococcus abyssi
 C>Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 09-Jul-2004
 C:Accession: A75088

R:Anonymous, Genoscope
 submitted to the EMBL Data Library, July 1999
 A:Description: Pyrococcus abyssi genome sequence: insights into archaeal chromosome stru
 A:Reference number: A75001
 A:Accession: A75088
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-219 <KAW>
 A:Cross-references: UNIPROT:Q9UZQ0; UNIPARC:UPI00000633B1; GB:AJ248286; GB:AL096836; NID
 A:Experimental source: strain Orsay
 C:Genetics:
 A:Gene: PAB1640

Query Match 50.6%; Score 40; DB 2; Length 219;
 Best Local Similarity 53.8%; Pred. NO. 11;
 Matches 7; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1 RHYGETKMNQRS 13
 :||| |:
 DB 12 KHYGETVLIENS 24

Search completed: April 21, 2006, 13:42:31
 Job time : 54 secs

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OM protein - protein search, using sw model

Run on: April 21, 2006, 13:34:25 ; Search time 230 Seconds

(without alignment)

46.013 Million cell updates/sec

Title: US-09-993-399-1

Perfect score: 79

Sequence: 1 RHYGETKMQRSRS 15

Scoring table: BLOSOM62

Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1000 summaries

Database : Uniprot_05.80:*

1: uniprot_sprot:*

2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	79	100.0	2585	Q4LE75_HUMAN	Q4LE75 homo sapien
2	79	100.0	2663	CENPE_HUMAN	Q02224 homo sapien
3	75	94.9	1558	Q4SEM9_TETNG	Q4SEM9 tetraodon n
4	71	89.9	160	O35059_MOUSE	O35059 mus musculus
5	71	89.9	549	Q7TPX4_MOUSE	Q7TPX4 mus musculus
6	71	89.9	2474	Q6RT24_MOUSE	Q6RT24 mus musculus
7	69	87.3	2954	Q42263_XENLA	Q42263 xenopus lae
8	58	73.4	807	Q94HV9_ARATH	Q94HV9 arabidopsis
9	58	73.4	823	Q9S7P3_ARATH	Q9S7P3 arabidopsis
10	58	73.4	888	Q9LQ62_ARATH	Q9LQ62 arabidopsis
11	54	68.4	842	Q7Q5F1_ANOGA	Q7Q5F1 anopheles g
12	54	68.4	859	Q6IWZ2_LEIDO	Q6IWZ2 leishmania
13	54	68.4	890	Q6IWZ1_LEIDO	Q6IWZ1 leishmania
14	54	68.4	955	KINL_LEICH	P46865 leishmania
15	54	68.4	1803	Q57UD0_9TRYP	Q57UD0 trypanosoma
16	53	67.1	578	Q57V46_9TRYP	Q57V46 trypanosoma
17	53	67.1	591	Q57V47_9TRYP	Q57V47 trypanosoma
18	53	67.1	1229	Q4QFM3_LEIMA	Q4QFM3 leishmania
19	53	67.1	2013	Q9VKI0_DROME	Q9VKI0 drosophila
20	53	67.1	2244	Q9NCG0_DROME	Q9NCG0 drosophila
21	53	67.1	2765	Q4QFM4_LEIMA	Q4QFM4 leishmania
22	53	67.1	2976	Q4QFM2_LEIMA	Q4QFM2 leishmania
23	53	65.8	168	Q54722_RAT	Q54722 rattus norv
24	52	65.8	459	Q9SS30_ARATH	Q9SS30 arabidopsis
25	52	65.8	810	Q57XT2_9TRYP	Q57XT2 trypanosoma
26	52	65.8	865	Q9SILL1_MACFA	Q9SILL1 macaca fasc
27	52	65.8	1266	Q7PCK6_MACFA	Q7PCK6 macaca fasc
28	52	65.8	1304	Q86VH0_HUMAN	Q86VH0 homo sapien
29	52	65.8	1335	Q86VH1_HUMAN	Q86VH1 homo sapien
30	52	65.8	1394	Q7M6Z5_RAT	Q7M6Z5 rattus norv
31	52	65.8	1394	Q7M6Z4_MOUSE	Q7M6Z4 mus musculus

32	65.8	1401	2	Q86VH2_HUMAN	Q86VH2 homo sapien
33	65.8	1931	2	Q9NCF9_DROME	Q9NCF9 drosophila
34	65.8	1931	2	Q9VKH9_DROME	Q9VKH9 drosophila
35	51	581	2	Q9SVU7_ARATH	Q9SVU7 arabidopsis
36	51	64.6	834	Q9SVJ8_ARATH	Q9SVJ8 arabidopsis
37	50	63.3	777	Q5VRK9_DROME	Q5VRK9 drosophila
38	50	63.3	746	Q57ZAG_9TRYP	Q57ZAG trypanosoma
39	50	63.3	1043	Q4P5T9_USTMA	Q4P5T9 ustilago ma
40	50	63.3	1459	Q4PG67_USTMA	Q4PG67 ustilago ma
41	50	63.3	1459	P87198_USTMA	P87198 ustilago ma
42	50	63.3	1624	Q9U679_STRPU	Q9U679 strongyloce
43	49	62.0	146	Q91113_MORSA	Q91113 morone saxa
44	49	62.0	148	Q35232_MOUSE	Q35232 mus musculus
45	49	62.0	156	O15719_DICDI	O15719 dictyosteli
46	49	62.0	193	Q84JL8_ARATH	Q84JL8 arabidopsis
47	49	62.0	198	Q9MAU7_ARATH	Q9MAU7 arabidopsis
48	49	62.0	573	Q4SIJ2_TETNG	Q4SIJ2 tetraodon n
49	49	62.0	597	Q5R9A3_PONPY	Q5R9A3 pongo pygma
50	49	62.0	600	Q4R838_MACFA	Q4R838 macaca fasc
51	49	62.0	660	Q99LC7_MOUSE	Q99LC7 mus musculus
52	49	62.0	665	K1P22_HUMAN	K1P222 homo sapien
53	49	62.0	665	Q53F58_HUMAN	Q53F58 homo sapien
54	49	62.0	665	Q5REP4_PONPY	Q5REP4 pongo pygma
55	49	62.0	1363	Q58G59_BRARE	Q58G59 brachydanio
56	49	62.0	1885	Q869B8_DICDI	Q869B8 dictyosteli
57	49	62.0	1922	Q54NP8_DICDI	Q54NP8 dictyosteli
58	48	60.8	170	Q9AVD7_TOBAC	Q9AVD7 nicotiana t
59	48	60.8	406	Q4SKM2_TETNG	Q4SKM2 tetraodon n
60	48	60.8	657	Q510E8_RAT	Q510E8 rattus norv
61	48	60.8	862	Q851Z7_ORYSA	Q851Z7 oryza sativ
62	48	60.8	925	Q7YVJ8_CRYPV	Q7YVJ8 cryptospori
63	48	60.8	934	Q5CJ33_CRYHO	Q5CJ33 cryptospori
64	48	60.8	1034	Q4QDF2_LEIMA	Q4QDF2 leishmania
65	48	60.8	1061	Q4QDF3_LEIMA	Q4QDF3 leishmania
66	48	60.8	1062	Q4Q9P4_LEIMA	Q4Q9P4 leishmania
67	48	60.8	1070	Q9SV36_ARATH	Q9SV36 arabidopsis
68	48	60.8	1254	Q4QJC6_LEIMA	Q4QJC6 leishmania
69	48	60.8	2078	Q4Q3T1_LEIMA	Q4Q3T1 leishmania
70	47	59.5	347	Q93XF8_MAIZE	Q93XF8 zea mays (m
71	47	59.5	672	Q9GV93_CABER	Q9GV93 caenorhabdi
72	47	59.5	686	Q61HG5_CABER	Q61HG5 caenorhabdi
73	47	59.5	699	QSM3_CABER	QSM3 caenorhabdi
74	47	59.5	754	ATK3_ARATH	P46875 arabidopsis
75	47	59.5	793	ATK1_ARATH	Q07970 arabidopsis
76	47	59.5	956	Q9GRN3_LEIMA	Q9GRN3 leishmania
77	47	59.5	990	Q8T135_DICDI	Q8T135 dictyosteli
78	46	58.2	102	Q8XB88_ECO57	Q8XB88 escherichia
79	46	58.2	108	Q7ACV4_ECO57	Q7ACV4 escherichia
80	46	58.2	121	YEDR_ECOLI	P76134 escherichia
81	46	58.2	127	Q8FGJ0_ECOL6	Q8FGJ0 escherichia
82	46	58.2	145	Q91115_MORSA	Q91115 morone saxa
83	46	58.2	465	Q8LXJ3_ARATH	Q8LXJ3 arabidopsis
84	46	58.2	469	Q8LEG9_ARATH	Q8LEG9 arabidopsis
85	46	58.2	818	Q7XN65_ORYSA	Q7XN65 oryza sativ
86	46	58.2	824	Q4SUU7_TETNG	Q4SUU7 tetraodon n
87	46	58.2	928	Q4REL2_TETNG	Q4REL2 tetraodon n
88	46	58.2	932	Q9LXL3_ARATH	Q9LXL3 arabidopsis
89	46	58.2	937	Q8LGU3_ARATH	Q8LGU3 arabidopsis
90	46	58.2	937	Q8L5J2_ARATH	Q8L5J2 arabidopsis
91	46	58.2	938	Q8L2Z2_ARATH	Q8L2Z2 arabidopsis
92	46	58.2	955	Q8S949_TOBAC	Q8S949 nicotiana t
93	46	58.2	958	Q969B4_GIALA	Q969B4 giardia lam
94	46	58.2	1066	Q7QVT8_GIALA	Q7QVT8 giardia lam
95	46	58.2	1107	Q5J2U3_9CHLO	Q5J2U3 stichococu
96	46	58.2	1209	Q7Y1U0_GOSHI	Q7Y1U0 gosyplum h
97	45	57.0	145	Q91117_MORSA	Q91117 morone saxa
98	45	57.0	145	Q91114_MORSA	Q91114 morone saxa
99	45	57.0	145	Q91110_MORSA	Q91110 morone saxa
100	45	57.0	238	K1F5C_RAT	P56536 rattus norv
101	45	57.0	315	Q927U3_LISIN	Q927U3 listeria in
102	45	57.0	315	Q91RNO_LISMO	Q91RNO listeria mo
103	45	57.0	317	Q9GMV1_MACFA	Q9GMV1 macaca fasc
104	45	57.0	345	Q6P164_HUMAN	Q6P164 homo sapien

105	45	57.0	346	2	Q5REP7_PONPY	Q5rep7 pongo pygma	178	44	55.7	782	2	Q9GV92_CAEEL	Q9gv92 caenorhabdi
106	45	57.0	349	2	Q8CFE7_MOUSE	Q8cfe7 mus musculus	179	44	55.7	897	2	Q93XF3_MAIZE	Q93xf3 zea mays (m
107	45	57.0	349	2	Q504B9_BRARE	Q504b9 brachydanio	180	44	55.7	918	2	Q6F301_ORYSA	Q6f301 oryza sativ
108	45	57.0	351	2	Q6PJ44_HUMAN	Q6pj44 homo sapien	181	44	55.7	971	2	Q5JKW1_ORYSA	Q5jkw1 oryza sativ
109	45	57.0	351	2	Q66K46_HUMAN	Q66k46 homo sapien	182	44	55.7	987	2	Q9C9A8_ARATH	Q9c9a8 arabidopsis
110	45	57.0	351	2	Q6NS55_MOUSE	Q6ns55 mus musculus	183	44	55.7	1050	2	Q9C9S6_ARATH	Q9c9s6 arabidopsis
111	45	57.0	352	2	Q6PKD1_HUMAN	Q6pkd1 homo sapien	184	44	55.7	1130	2	Q8MQ88_CAEEL	Q8mq88 caenorhabdi
112	45	57.0	354	2	Q93XF5_MAIZE	Q93xf5 zea mays (m	185	44	55.7	1172	2	Q7QSR2_GIALA	Q7qsr2 giardia lam
113	45	57.0	358	2	Q6NNT8_DROME	Q6nnt8 drosophila	186	44	55.7	1463	2	Q7XJW0_ORYSA	Q7xjw0 oryza sativ
114	45	57.0	394	2	Q7XALI_ORYSA	Q7xali oryza sativ	187	44	55.7	2221	2	Q4QDF1_LEIMA	Q4qdf1 leishmania
115	45	57.0	590	2	Q6VL14_COTCO	Q6vl14 coturnix co	188	43	54.4	268	2	Q5W4S8_CHICK	Q5w4s8 gallus gall
116	45	57.0	642	2	Q7YL88_ORYSA	Q7yl88 oryza sativ	189	43	54.4	305	2	Q6PLD3_MOUSE	Q6pld3 mus musculu
117	45	57.0	745	1	ATK2_ARATH	P46864 arabidopsis	190	43	54.4	310	2	Q4SJV4_TETNG	Q4sjv4 tetraodon n
118	45	57.0	766	2	Q93XG3_MAIZE	Q93xg3 zea mays (m	191	43	54.4	408	2	Q8IWH8_HUMAN	Q8iwh8 homo sapien
119	45	57.0	777	2	Q9M0X6_ARATH	Q9m0x6 arabidopsis	192	43	54.4	408	2	Q8OUK1_MOUSE	Q8ouk1 mus musculu
120	45	57.0	790	2	Q6NQ77_ARATH	Q6nq77 arabidopsis	193	43	54.4	425	2	Q94JU6_ARATH	Q94ju6 arabidopsis
121	45	57.0	820	2	Q6GSA9_9TRYP	Q6gsa9 trypanosoma	194	43	54.4	443	2	Q8CGJ1_MOUSE	Q8cgj1 mus musculu
122	45	57.0	884	2	Q6H638_ORYSA	Q6h638 oryza sativ	195	43	54.4	447	2	Q6DCF1_YENLA	Q6dcf1 xenopus lae
123	45	57.0	916	2	Q4SNN2_TETNG	Q4snn2 tetraodon n	196	43	54.4	449	2	Q6DEG6_BRARE	Q6deg6 brachydanio
124	45	57.0	950	2	Q7PG43_ANOGA	Q7pg43 anopheles g	197	43	54.4	482	2	Q6IC70_CABBR	Q6ic70 caenorhabdi
125	45	57.0	956	1	KIF5C_MOUSE	P28738 mus musculu	198	43	54.4	569	2	Q4R4B6_MACFA	Q4r4b6 macaca faec
126	45	57.0	956	2	Q6NX19_MOUSE	Q6nx19 mus musculu	199	43	54.4	698	2	Q5SX84_MOUSE	Q5sx84 mus musculu
127	45	57.0	957	1	KIF5C_HUMAN	P60282 homo sapien	200	43	54.4	699	2	Q98T11_XENLA	Q98t11 xenopus lae
128	45	57.0	963	1	KINH_HUMAN	P33176 homo sapien	201	43	54.4	701	1	KIF3A_MOUSE	P28741 mus musculu
129	45	57.0	963	1	KINH_MOUSE	P61768 mus musculu	202	43	54.4	702	2	Q7TSZ7_MOUSE	Q7tsz7 mus musculu
130	45	57.0	963	2	Q5VZ85_HUMAN	Q5vz85 homo sapien	203	43	54.4	702	1	KIF3A_HUMAN	Q9y496 homo sapien
131	45	57.0	963	2	Q5BL10_MOUSE	Q5bl10 mus musculu	204	43	54.4	702	2	Q5R4H3_PONPY	Q5r4h3 pongo pygma
132	45	57.0	967	1	KINH_LOLPE	P21613 loligo peal	205	43	54.4	702	2	Q4R628_MACFA	Q4r628 macaca faec
133	45	57.0	975	1	KINH_DROME	P17210 drosophila	206	43	54.4	706	2	Q5F3C2_CHICK	Q5f3c2 gallus gall
134	45	57.0	986	2	Q6Z9D1_ORYSA	Q6z9d1 oryza sativ	207	43	54.4	728	2	Q4SJV3_TETNG	Q4sjv3 tetraodon n
135	45	57.0	987	2	Q6CHF1_MOUSE	Q6chf1 mus musculu	208	43	54.4	730	2	Q59EN1_HUMAN	Q59en1 homo sapien
136	45	57.0	998	2	Q6C348_YARLI	Q6c348 yarrowia li	209	43	54.4	739	2	Q5F423_CHICK	Q5f423 gallus gall
137	45	57.0	1003	2	Q6Z9D2_ORYSA	Q6z9d2 oryza sativ	210	43	54.4	744	2	Q93478_XENLA	Q93478 xenopus lae
138	45	57.0	1027	1	KINN_MOUSE	P33175 mus musculu	211	43	54.4	747	1	KIF3B_HUMAN	O15066 homo sapien
139	45	57.0	1027	2	Q6OLM7_RAT	Q6olm7 rattus norv	212	43	54.4	747	1	KIF3B_MOUSE	Q61771 mus musculu
140	45	57.0	1027	2	Q6PDY7_MOUSE	Q6pyd7 mus musculu	213	43	54.4	747	2	Q8BNH4_MOUSE	Q8bnh4 mus musculu
141	45	57.0	1031	1	KINH_STRPU	P35978 strongyloce	214	43	54.4	757	2	Q8OU27_MOUSE	Q8ou27 mus musculu
142	45	57.0	1032	1	KINN_HUMAN	Q12840 homo sapien	215	43	54.4	765	2	Q93XG2_MAIZE	Q93xg2 zea mays (m
143	45	57.0	1032	2	Q5R9K7_PONPY	Q5r9k7 pongo pygma	216	43	54.4	767	2	Q22240_ARATH	Q22240 arabidopsis
144	45	57.0	1040	2	Q4S807_TETNG	Q4s807 tetraodon n	217	43	54.4	776	2	Q4T9W2_TETNG	Q4t9w2 tetraodon n
145	45	57.0	1043	2	Q4LE26_HUMAN	Q4le26 homo sapien	218	43	54.4	786	1	FLA10_CHLRE	P46869 chlamydomon
146	45	57.0	1060	2	Q4TBE0_TETNG	Q4tbe0 tetraodon n	219	43	54.4	810	2	Q7ZUR2_BRARE	Q7zur2 brachydanio
147	45	57.0	1064	2	Q4S869_TETNG	Q4s869 tetraodon n	220	43	54.4	903	2	Q4XNS6_PLACH	Q4xns6 plasmodium
148	45	57.0	1105	2	Q5KE89_CRYNE	Q5ke89 cryptococcu	221	43	54.4	915	2	Q7FBI7_ORYSA	Q7fbi7 oryza sativ
149	45	57.0	1158	2	Q5DTP1_MOUSE	Q5dtp1 mus musculu	222	43	54.4	945	2	Q7X7H4_ORYSA	Q7x7h4 oryza sativ
150	45	57.0	1207	2	Q5SP68_CRYNE	Q5sp68 cryptococcu	223	43	54.4	954	2	Q9AMW8_ORYSA	Q9awm8 oryza sativ
151	45	57.0	1259	2	Q22326_ARATH	Q22326 arabidopsis	224	43	54.4	959	2	Q8S950_TOBAC	Q8s950 nicotiana t
152	45	57.0	1259	2	Q23102_ARATH	Q23102 arabidopsis	225	43	54.4	968	2	Q8SD31_ARATH	Q8sd31 arabidopsis
153	45	57.0	1260	2	Q9FHN8_ARATH	Q9fhn8 arabidopsis	226	43	54.4	974	2	Q8S905_ARATH	Q8s905 arabidopsis
154	45	57.0	1261	2	Q39130_ARATH	Q39130 arabidopsis	227	43	54.4	995	2	Q22974_ARATH	Q22974 arabidopsis
155	44	55.7	158	2	Q9FQL8_CYAPA	Q9fq18 cyanophora	228	43	54.4	1003	2	Q9LPQ5_ARATH	Q9lpq5 arabidopsis
156	44	55.7	264	2	Q569C0_GIALA	Q569c0 giardia lam	229	43	54.4	1037	2	Q9FH58_ARATH	Q9fh58 arabidopsis
157	44	55.7	325	2	Q5J2U2_CYAPA	Q5j2u2 cyanophora	230	43	54.4	1041	2	Q57XU6_9TRYP	Q57xu6 trypanosoma
158	44	55.7	328	2	Q93XG3_MAIZE	Q93xg1 zea mays (m	231	43	54.4	1056	2	Q9C9C9_ARATH	Q9c9c9 arabidopsis
159	44	55.7	405	2	Q93XF2_MAIZE	Q93xf2 zea mays (m	232	43	54.4	1087	2	Q9F1G8_ARATH	Q9f1g8 arabidopsis
160	44	55.7	438	2	Q5Z9S9_ORYSA	Q5z9s9 oryza sativ	233	43	54.4	1109	2	Q8W1Y3_ARATH	Q8w1y3 arabidopsis
161	44	55.7	447	2	Q6OKW3_CABBR	Q6okw3 caenorhabdi	234	43	54.4	1227	2	Q4QJ47_ARATH	Q4qjd7 arabidopsis
162	44	55.7	557	2	Q7PQZ7_ANOGA	Q7pqz7 anopheles g	235	43	54.4	1263	2	Q4SHD9_LEIMA	Q4shd9 leishmania
163	44	55.7	561	2	Q7SUP8_IPOBA	Q7sup8 ipomoea bat	236	43	54.4	1263	2	Q9SU42_ARATH	Q9su42 arabidopsis
164	44	55.7	589	2	Q4FXG3_LEIMA	Q4fxg3 leishmania	237	43	54.4	1342	2	Q57YB0_9TRYP	Q57yb0 trypanosoma
165	44	55.7	590	2	Q4FXG4_LEIMA	Q4fxg4 leishmania	238	43	54.4	1661	2	Q4Z625_PLABE	Q4z625 plasmodium
166	44	55.7	607	2	Q9U5H3_CAEEL	Q9u5h3 caenorhabdi	239	43	54.4	1673	2	Q560K9_CRYNE	Q560k9 cryptococcu
167	44	55.7	619	2	Q969C9_GIALA	Q969c9 giardia lam	240	43	54.4	1844	2	Q8ISU0_PLAF7	Q8isu0 plasmodium
168	44	55.7	625	2	Q7QSW5_GIALA	Q7qsw5 giardia lam	241	43	54.4	1961	2	Q4QCT7_LEIMA	Q4qct7 leishmania
169	44	55.7	658	2	Q6CRW2_KJULA	Q6crw2 kluveromyc	242	43	54.4	2013	2	Q7RLW2_PLAYO	Q7rlw2 plasmodium
170	44	55.7	685	1	KIF2_ASHGO	Q81jg1 ashbya gos	243	43	54.4	2756	2	Q9LJ60_ARATH	Q9lj60 arabidopsis
171	44	55.7	685	2	Q6S001_DICTDI	Q6s001 dictyosteli	244	42	53.2	150	2	Q9AVD6_TOBAC	Q9avd6 nicotiana t
172	44	55.7	706	1	KIP2_YEAST	P28743 saccharomyc	245	42	53.2	157	2	Q9AVD2_TOBAC	Q9avd2 nicotiana t
173	44	55.7	718	2	Q7R485_GIALA	Q7r485 giardia lam	246	42	53.2	168	2	Q35068_MOUSE	Q35068 mus musculu
174	44	55.7	735	2	Q9U0D5_TETTH	Q9u0d5 tetrahymena	247	42	53.2	185	2	Q5DAN3_SCHJA	Q5dan3 schistosoma
175	44	55.7	742	1	KRP95_STRPU	P46871 strongyloce	248	42	53.2	407	2	Q93XF9_WAIZE	Q93xf9 zea mays (m
176	44	55.7	742	2	Q7M453_STRDR	Q7m453 strongyloce	249	42	53.2	415	2	Q95U25_DROME	Q95u25 drosophila
177	44	55.7	782	2	Q19633_CAEEL	Q19633 caenorhabdi	250	42	53.2	547	2	Q8Y252_ORYSA	Q8y252 oryza sativ

251	42	53.2	573	2	Q67L22_SYMTH	Q67L22 symbiobacte	324	40	50.6	168	2	Q8GW1_ARATH	Q8GW1 arabidopsia
252	42	53.2	631	2	Q6RPG0_XENLA	Q6RPG0 xenopus lae	325	40	50.6	168	2	Q8LF15_ARATH	Q8LF15 arabidopsia
253	42	53.2	638	2	Q58210_9TRYP	Q58210 trypanosoma	326	40	50.6	172	2	Q9AVD5_TORAC	Q9AVD5 nicotiana t
254	42	53.2	639	2	Q6P3R1_XENLA	Q6P3R1 xenopus tro	327	40	50.6	202	2	Q9XEB6_ARATH	Q9XEB6 arabidopsia
255	42	53.2	650	2	Q919A8_XENLA	Q919A8 xenopus lae	328	40	50.6	219	2	Q9UZQ0_PYRAB	Q9UZQ0 pyrococcus
256	42	53.2	651	2	Q918K0_XENLA	Q918K0 xenopus lae	329	40	50.6	248	2	Q4WMB9_ASFFU	Q4WMB9 aspergillus
257	42	53.2	651	2	Q91869_XENLA	Q91869 xenopus lae	330	40	50.6	302	2	Q8NLB0_CORGL	Q8NLB0 corynebacte
258	42	53.2	663	2	Q72YL5_XENLA	Q72YL5 xenopus lae	331	40	50.6	305	2	Q8M1H8_CORGL	Q8M1H8 corynebacte
259	42	53.2	681	2	Q5J2U4_PICAB	Q5J2U4 picea abies	332	40	50.6	332	2	Q7Q1P1_ANOGA	Q7Q1P1 anopheles g
260	42	53.2	699	1	KRP85_STRPU	K46872 strongyloce	333	40	50.6	353	2	Q503Q4_BRARE	Q503Q4 brachydanio
261	42	53.2	702	2	Q6FRP9_CANGA	Q6FRP9 candida gla	334	40	50.6	452	2	Q8R471_RAT	Q8R471 rattus norv
262	42	53.2	738	1	K1FC2_HUMAN	Q96AC6 homo sapien	335	40	50.6	480	2	Q8C901_MOUSE	Q8C901 mus musculu
263	42	53.2	861	2	Q22260_ARATH	Q22260 arabidopsia	336	40	50.6	481	2	Q8BNG3_MOUSE	Q8BNG3 mus musculu
264	42	53.2	889	2	Q703G7_EMENI	Q703G7 emericella	337	40	50.6	486	2	Q54720_RAT	Q54720 rattus norv
265	42	53.2	889	2	Q5ATU4_EMENI	Q5ATU4 aspergillus	338	40	50.6	535	2	Q17340_CABEL	Q17340 caenorhabdi
266	42	53.2	955	2	Q4WG42_ASFFU	Q4WG42 aspergillus	339	40	50.6	538	2	Q7PVB7_HUMAN	Q7PVB7 anopheles g
267	42	53.2	956	2	Q9C7B9_ARATH	Q9C7B9 arabidopsia	340	40	50.6	548	2	Q5T8B0_HOMO	Q5T8B0 homo sapien
268	42	53.2	983	2	Q84W97_ARATH	Q84W97 arabidopsia	341	40	50.6	578	2	Q87GW9_VTBPA	Q87GW9 vibrio para
269	42	53.2	997	2	Q8FG03_ARATH	Q8FG03 arabidopsia	342	40	50.6	581	2	Q8ZYMO_PYRAB	Q8ZYMO pyrobaculum
270	42	53.2	1003	2	Q7X934_VOLCA	Q7X934 volvox cart	343	40	50.6	629	2	Q51EX3_ENTHI	Q51EX3 entamoeba h
271	42	53.2	1009	2	Q7X931_CHLRE	Q7X931 chlamydomon	344	40	50.6	672	2	Q6FK03_CANGA	Q6FK03 candida gla
272	42	53.2	1033	2	Q91LH9_ARATH	Q91LH9 arabidopsia	345	40	50.6	721	2	Q7QDS6_ANOGA	Q7QDS6 anopheles g
273	42	53.2	1200	2	Q9FOL7_MAIZE	Q9FOL7 zea mays (m	346	40	50.6	773	1	Q6CC36_YARLI	Q6CC36 yarrowia li
274	42	53.2	1218	2	Q9V646_DROME	Q9V646 drosophila	347	40	50.6	784	2	KLP68_DROME	P46867 drosophila
275	42	53.2	1260	2	Q8VZV4_ARATH	Q8VZV4 arabidopsia	348	40	50.6	784	2	Q961H5_DROME	Q961H5 drosophila
276	42	53.2	1665	2	Q4FXV7_LEIMA	Q4FXV7 leishmania	349	40	50.6	814	1	CF102_HUMAN	Q82MV9 homo sapien
277	42	53.2	1801	2	Q5K8T9_CRYNE	Q5K8T9 cryptococcu	350	40	50.6	819	2	Q55HQ7_CRYNE	Q55HQ7 cryptococcu
278	42	53.2	1801	2	Q55LY0_CRYNE	Q55LY0 cryptococcu	351	40	50.6	819	2	Q5K793_CRYNE	Q5K793 cryptococcu
279	42	51.9	157	2	Q9AVD9_TOBAC	Q9AVD9 nicotiana t	352	40	50.6	881	2	Q5ZKH9_CHICK	Q5ZKH9 gallus gall
280	41	51.9	204	2	Q5TV22_ANOGA	Q5TV22 anopheles g	353	40	50.6	897	2	Q60ZS0_CAEBR	Q60ZS0 caenorhabdi
281	41	51.9	383	2	Q95XME_CABEL	Q95XME caenorhabdi	354	40	50.6	897	2	Q8S842_ARATH	Q8S842 arabidopsia
282	41	51.9	458	2	Q5OR62_ENTHI	Q5OR62 entamoeba h	355	40	50.6	920	2	Q8ABX7_BACTN	Q8ABX7 bacteroides
283	41	51.9	570	2	Q9YDG3_AERPE	Q9YDG3 aeropyrum p	356	40	50.6	962	2	Q9FHD2_ARATH	Q9FHD2 arabidopsia
284	41	51.9	593	2	Q5FKC4_LACAC	Q5FKC4 lactobacilli	357	40	50.6	1047	2	Q55KA5_CRYNE	Q55KA5 cryptococcu
285	41	51.9	593	2	Q61B82_CAEBR	Q61B82 caenorhabdi	358	40	50.6	1048	2	Q9NGN7_DROME	Q9NGN7 drosophila
286	41	51.9	605	2	Q4XPJ5_PLACH	Q4XPJ5 plasmodium	359	40	50.6	1049	2	Q9VKM4_DROME	Q9VKM4 drosophila
287	41	51.9	614	2	Q84VC0_ORYSA	Q84VC0 oryza sativ	360	40	50.6	1049	2	Q5K997_CRYNE	Q5K997 cryptococcu
288	41	51.9	635	2	Q759X8_ASHGO	Q759X8 ashbya gos	361	40	50.6	1051	2	Q94LW7_ARATH	Q94LW7 arabidopsia
289	41	51.9	697	2	Q9U921_TETTH	Q9U921 tetrahymena	362	40	50.6	1075	2	Q2SNE3_ARATH	Q2SNE3 arabidopsia
290	41	51.9	699	2	Q70AQ4_USTMA	Q70AQ4 ustilago ma	363	40	50.6	1142	1	G1N4_YEAST	Q12263 saccharomyc
291	41	51.9	763	2	Q5AZEO_EMENI	Q5AZEO aspergillus	364	40	50.6	1149	2	Q4YBS0_PLABE	Q4YBS0 plasmodium
292	41	51.9	768	2	Q57WJ5_9TRYP	Q57WJ5 trypanosoma	365	40	50.6	1191	2	Q8GZU1_LVCES	Q8GZU1 lycopersico
293	41	51.9	769	2	Q4X092_ASFFU	Q4X092 aspergillus	366	40	50.6	1194	2	Q7R321_GIALA	Q7R321 giardia lam
294	41	51.9	770	1	KLPA_EMENI	P28739 emericella	367	40	50.6	1226	2	Q84VE4_ORYSA	Q84VE4 oryza sativ
295	41	51.9	787	2	Q57XZ5_9TRYP	Q57XZ5 trypanosoma	368	40	50.6	1248	2	Q7XPJ0_ORYSA	Q7XPJ0 oryza sativ
296	41	51.9	802	2	Q93928_NECHA	Q93928 nectria hae	369	40	50.6	1499	2	Q6S000_DICDI	Q6S000 dictyosteli
297	41	51.9	802	2	Q41L54_GIBZE	Q41L54 gibberella	370	40	50.6	1671	2	Q54M02_DICDI	Q54M02 dictyosteli
298	41	51.9	830	2	Q872F6_NEUCR	Q872F6 neuropora	371	40	50.6	2248	2	Q4P906_USTMA	Q4P906 ustilago ma
299	41	51.9	832	1	KLP1_SCHPO	Q92376 schizosach	372	40	50.6	2743	2	Q4SR36_TETNG	Q4SR36 tetraodon n
300	41	51.9	833	2	Q5AW68_EMENI	Q5AW68 aspergillus	373	39.5	50.0	692	2	Q8C9Y7_MOUSE	Q8C9Y7 mus musculu
301	41	51.9	839	2	Q4QDJ5_LEIMA	Q4QDJ5 leishmania	374	39.5	50.0	738	1	ECT2_MOUSE	Q07139 mus musculu
302	41	51.9	857	2	Q93XF4_MAIZE	Q93XF4 zea mays (m	375	39.5	50.0	882	2	Q80VE4_MOUSE	Q80VE4 mus musculu
303	41	51.9	871	2	Q4RF96_TETNG	Q4RF96 tetraodon n	376	39.5	50.0	882	2	Q8CIH2_MOUSE	Q8CIH2 mus musculu
304	41	51.9	887	1	K120A_MOUSE	P97329 mus musculu	377	39.5	50.0	882	2	Q8K2A0_MOUSE	Q8K2A0 mus musculu
305	41	51.9	887	2	Q542M4_MOUSE	Q542M4 mus musculu	378	39.5	50.0	913	2	Q8R3E2_MOUSE	Q8R3E2 mus musculu
306	41	51.9	924	2	Q86297_GIBMO	Q86297 gibberella	379	39.5	50.0	919	2	Q8DTR8_MOUSE	Q8DTR8 mus musculu
307	41	51.9	971	2	Q6YUL7_ORYSA	Q6YUL7 oryza sativ	380	39	49.4	33	2	Q7YV06_9TRYP	Q7YV06 trypanosoma
308	41	51.9	978	2	Q86ZC0_BOTCI	Q86ZC0 botrytis ci	381	39	49.4	144	2	Q512S0_ENTHI	Q512S0 entamoeba h
309	41	51.9	1012	2	Q528U1_MAGGR	Q528U1 magnaporthe	382	39	49.4	198	2	Q4PDX3_USTMA	Q4PDX3 ustilago ma
310	41	51.9	1032	2	Q9FIJ9_ARATH	Q9FIJ9 arabidopsia	383	39	49.4	216	2	Q80JV8_PICCO	Q80JV8 foot-and-no
311	41	51.9	1035	2	Q6YUL8_ORYSA	Q6YUL8 oryza sativ	384	39	49.4	225	2	Q8HYX6_HUMAN	Q8HYX6 homo sapien
312	41	51.9	1035	2	Q8GS71_ARATH	Q8GS71 arabidopsia	385	39	49.4	291	2	Q4KPC9_CANFA	Q4KPC9 canis famli
313	41	51.9	1084	2	Q4P5V6_USTMA	Q4P5V6 ustilago ma	386	39	49.4	292	1	SHOX_HUMAN	O15266 homo sapien
314	41	51.9	1129	2	Q5W6L9_ORYSA	Q5W6L9 oryza sativ	387	39	49.4	292	2	Q5HYX7_HUMAN	Q5HYX7 homo sapien
315	41	51.9	1189	2	Q81825_DICDI	Q81825 dictyosteli	388	39	49.4	292	2	Q5IT45_HUMAN	Q5IT45 homo sapien
316	41	51.9	1193	2	Q6S005_DICDI	Q6S005 dictyosteli	389	39	49.4	340	2	Q9IAZ0_9PERC	Q9IAZ0 spherooides
317	41	51.9	1193	2	Q54UC9_DICDI	Q54UC9 dictyosteli	390	39	49.4	340	2	Q9IAZ6_9PERC	Q9IAZ6 spherooides
318	41	51.9	1257	2	Q4QBQ1_LEIMA	Q4QBQ1 leishmania	391	39	49.4	341	2	Q4RT97_TETNG	Q4RT97 tetraodon n
319	41	51.9	1265	2	Q24147_TOBAC	Q24147 nicotiana t	392	39	49.4	365	2	Q6G474_BARHE	Q6G474 bartonella
320	41	51.9	1265	2	Q41460_SOLTU	Q41460 solanum tub	393	39	49.4	437	2	Q9Y013_PLAF7	Q9Y013 plasmodium
321	41	51.9	1335	2	Q9FME7_ARATH	Q9FME7 arabidopsia	394	39	49.4	444	2	Q6BY68_DEBHA	Q6BY68 debaryomyce
322	41	51.9	1394	2	Q582P0_9TRYP	Q582P0 trypanosoma	395	39	49.4	445	2	Q4LJ90_9BURK	Q4LJ90 burkholderi
323	40	50.6	165	2	Q35067_MOUSE	Q35067 mus musculu	396	39	49.4	447	1	ENGA_RALUSO	Q8Y026 raietonia s

397	39	49.4	447	2	Q55521_SVNY3	Q55521_synechocyst	470	38	48.1	158	2	Q9L0S2_STRCO	Q9L0S2 streptomyce
398	39	49.4	451	2	Q7U6Z7_SVNPX	Q7U6z7 synechococc	471	38	48.1	166	2	O35065_MOUSE	O35065 mus musculu
399	39	49.4	474	2	Q8R35_ENCCU	Q8r35 synechalito	472	38	48.1	183	1	SCPB_STRP3	P60222 streptococc
400	39	49.4	497	2	Q8R13_FUSN	Q8r13 fusobacteri	473	38	48.1	183	1	SCPB_STRP6	SCPB_STRP6 streptococ
401	39	49.4	540	2	Q4N4F5_THEPA	Q4n4f5 theileria p	474	38	48.1	183	1	SCPB_STRP8	P60211 streptococ
402	39	49.4	547	2	Q4UF42_THEAN	Q4uf42 theileria a	475	38	48.1	183	1	SCPB_STRPY	P60220 streptococ
403	39	49.4	548	2	Q416L5_GIBZE	Q416l5 gibberella	476	38	48.1	187	2	Q4RNK2_TETNG	Q4rnk2 tetradodon n
404	39	49.4	548	2	Q8SQOU_ENCCU	Q8sqou encephalito	477	38	48.1	188	2	RASN_BRARE	P79737 brachydanio
405	39	49.4	563	2	Q526P0_MAGGR	Q526p0 magnaporthe	478	38	48.1	188	2	O6DGD1_BRARE	Q6dgd1 brachydanio
406	39	49.4	598	2	Q86Z44_COCHE	Q86z44 cochllobolu	479	38	48.1	218	2	O4LM35_9BURK	Q4lm35 burkholderi
407	39	49.4	603	2	Q86ZB0_COCHE	Q86zb0 cochllobolu	480	38	48.1	221	2	O24180_PEA	Q24180 pisum sativ
408	39	49.4	648	2	Q4R112_TETNG	Q4r112 tetradodon n	481	38	48.1	228	2	Q24180_9CNID	Q24180 eleutheria
409	39	49.4	661	2	Q86Z93_GIBMO	Q86z93 gibberella	482	38	48.1	237	1	SHOX2_RAT	Q35750 rattus norv
410	39	49.4	670	2	Q5AXW7_EMENI	Q5axw7 aspergillus	483	38	48.1	267	2	O4SSW1_TETNG	Q4ssw1 tetradodon n
411	39	49.4	676	2	Q8C2M3_NEUCR	Q8c2m3 neurospora	484	38	48.1	299	2	O4L780_9BURK	Q4l780 burkholderi
412	39	49.4	705	2	Q53SX5_HUMAN	Q53sx5 homo sapien	485	38	48.1	324	1	FABH_CAMJE	Q9p1h1 campylobact
413	39	49.4	777	2	Q4WVR5_ASFPF	Q4wvr5 aspergillus	486	38	48.1	324	2	O5HWE3_CAMJR	O5hwe3 campylobact
414	39	49.4	779	2	Q5KFC1_CRYNE	Q5kfc1 cryptococcu	487	38	48.1	325	2	O53716_STRAT	O53716 streptomyce
415	39	49.4	786	2	Q5SQU4_CRYNE	Q5squ4 cryptococcu	488	38	48.1	330	2	O9PSH9_XENLA	Q9psh9 xenopus lae
416	39	49.4	791	2	Q6CH93_YARLI	Q6ch93 yarrowia li	489	38	48.1	331	2	O61W7_ECOLI	Q61w7 escherichia
417	39	49.4	793	1	K1F3C_HUMAN	K1f3c homo sapien	490	38	48.1	331	1	MRW_SILPO	Q9rks1 streptomyce
418	39	49.4	793	2	Q7Z2W5_HUMAN	Q7z2w5 homo sapien	491	38	48.1	331	1	SHOX2_MOUSE	O69414 escherichia
419	39	49.4	793	2	Q562F7_HUMAN	Q562f7 homo sapien	492	38	48.1	331	1	SHOX2_MOUSE	P14633 escherichia
420	39	49.4	793	2	Q5R706_PONPY	Q5r706 pongo pygma	493	38	48.1	331	1	SHOX2_MOUSE	Q7rk19 plasmodium
421	39	49.4	796	1	K1F3C_MOUSE	K1f3c mus musculu	494	38	48.1	331	1	SHOX2_MOUSE	Q7nmp2 gloeobacter
422	39	49.4	796	1	K1F3C_RAT	K1f3c rattus norv	495	38	48.1	331	1	SHOX2_MOUSE	Q6ch02 yarrowia li
423	39	49.4	815	2	Q43273_HUMAN	Q43273 homo sapien	496	38	48.1	331	1	SHOX2_MOUSE	Q6cwx5 kluveromyc
424	39	49.4	832	2	Q571AC_MOUSE	Q571ac mus musculu	497	38	48.1	331	1	SHOX2_MOUSE	Q6c990 yarrowia li
425	39	49.4	836	2	Q7YUC7_TETTH	Q7yuc7 tetrahymena	498	38	48.1	331	1	SHOX2_MOUSE	Q4icr1 gibberella
426	39	49.4	875	2	Q5CFZ7_CRYHO	Q5cfz7 cryptospori	499	38	48.1	331	1	SHOX2_MOUSE	Q5p679 homo sapien
427	39	49.4	880	2	Q69SH2_ORYSA	Q69sh2 oryza sativ	500	38	48.1	331	1	SHOX2_MOUSE	Q58e23 entamoeba h
428	39	49.4	884	2	Q8GV57_ORYSA	Q8gv57 oryza sativ	501	38	48.1	331	1	SHOX2_MOUSE	O8suhi encephalito
429	39	49.4	885	1	LONH1_MAZE	P91647 zea mays (m	502	38	48.1	331	1	SHOX2_MOUSE	O5b940 aspergillus
430	39	49.4	886	2	Q6RS97_WHEAT	Q6rs97 triticum ae	503	38	48.1	331	1	SHOX2_MOUSE	O6k8r0 oryza sativ
431	39	49.4	904	2	Q5A3K5_CANAL	Q5a3k5 candida alb	504	38	48.1	331	1	SHOX2_MOUSE	Q7v4z0 prochloroco
432	39	49.4	928	1	Q9HES9_EMENI	Q9hes9 emericella	505	38	48.1	331	1	SHOX2_MOUSE	Q8aw22 drosophila
433	39	49.4	928	1	KINH_NEUCR	P48467 neurospora	506	38	48.1	331	1	SHOX2_MOUSE	Q9w3q4 drosophila
434	39	49.4	929	2	P78718_NECRA	P78718 nectria hae	507	38	48.1	331	1	SHOX2_MOUSE	Q4p4g8 ustilago ma
435	39	49.4	929	2	Q4WLA6_ASFPF	Q4wla6 aspergillus	508	38	48.1	331	1	SHOX2_MOUSE	O6tgcx3 brachydanio
436	39	49.4	930	2	Q9G6S8_CABEL	Q9g6s8 caenorhabdi	509	38	48.1	331	1	SHOX2_MOUSE	O6tgcx3 brachydanio
437	39	49.4	931	1	KINH_GIBMO	Q86z98 gibberella	510	38	48.1	331	1	SHOX2_MOUSE	O6tgcx3 brachydanio
438	39	49.4	932	2	Q17753_CABEL	Q17753 caenorhabdi	511	38	48.1	331	1	SHOX2_MOUSE	O6tgcx3 brachydanio
439	39	49.4	939	2	Q1FCH0_GIBZE	Q1fch0 gibberella	512	38	48.1	331	1	SHOX2_MOUSE	O6tgcx3 brachydanio
440	39	49.4	945	1	C1N8_ASHGO	Q811g7 ashbya goss	513	38	48.1	331	1	SHOX2_MOUSE	O6tgcx3 brachydanio
441	39	49.4	957	2	O5CS61_CRYPV	O5cs61 cryptospori	514	38	48.1	331	1	SHOX2_MOUSE	O6tgcx3 brachydanio
442	39	49.4	965	2	Q6CSH2_KLULA	Q6csh2 kluveromyc	515	38	48.1	331	1	SHOX2_MOUSE	O6tgcx3 brachydanio
443	39	49.4	966	2	Q5B287_EMENI	Q5b287 aspergillus	516	38	48.1	331	1	SHOX2_MOUSE	O6tgcx3 brachydanio
444	39	49.4	970	2	Q9G9C6_GIALA	Q9g9c6 giardia lam	517	38	48.1	331	1	SHOX2_MOUSE	O6tgcx3 brachydanio
445	39	49.4	980	2	Q9NS55_HUMAN	Q9ns55 homo sapien	518	38	48.1	331	1	SHOX2_MOUSE	O6tgcx3 brachydanio
446	39	49.4	987	1	ATK4_ARATH	Q81635 arabidopsis	519	38	48.1	331	1	SHOX2_MOUSE	O6tgcx3 brachydanio
447	39	49.4	988	1	C1N8_CANGA	Q6fxi5 candida gla	520	38	48.1	331	1	SHOX2_MOUSE	O6tgcx3 brachydanio
448	39	49.4	1016	2	Q6FTD2_CANGA	Q6ftd2 candida gla	521	38	48.1	331	1	SHOX2_MOUSE	O6tgcx3 brachydanio
449	39	49.4	1019	2	Q5B5B4_EMENI	Q5b5b4 aspergillus	522	38	48.1	331	1	SHOX2_MOUSE	O6tgcx3 brachydanio
450	39	49.4	1022	2	Q9ZUS4_ARATH	Q9z4x6 gibberella	523	38	48.1	331	1	SHOX2_MOUSE	O6tgcx3 brachydanio
451	39	49.4	1038	1	C1N8_YEAST	Q52f79 magnaporthe	524	38	48.1	331	1	SHOX2_MOUSE	O6tgcx3 brachydanio
452	39	49.4	1045	2	Q9UNR9_HUMAN	Q51xe6 magnaporthe	525	38	48.1	331	1	SHOX2_MOUSE	O6tgcx3 brachydanio
453	39	49.4	1045	2	Q9NS56_HUMAN	Q9ns56 homo sapien	526	38	48.1	331	1	SHOX2_MOUSE	O6tgcx3 brachydanio
454	39	49.4	1045	2	Q6P987_HUMAN	Q6p987 homo sapien	527	38	48.1	331	1	SHOX2_MOUSE	O6tgcx3 brachydanio
455	39	49.4	1056	2	Q7RSP8_GIALA	Q7rsp8 giardia lam	528	38	48.1	331	1	SHOX2_MOUSE	O6tgcx3 brachydanio
456	39	49.4	1068	2	Q41PX6_GIBZE	Q41px6 gibberella	529	38	48.1	331	1	SHOX2_MOUSE	O6tgcx3 brachydanio
457	39	49.4	1070	2	Q52F79_MAGGR	Q52f79 magnaporthe	530	38	48.1	331	1	SHOX2_MOUSE	O6tgcx3 brachydanio
458	39	49.4	1108	2	Q51XE6_MAGGR	Q51xe6 magnaporthe	531	38	48.1	331	1	SHOX2_MOUSE	O6tgcx3 brachydanio
459	39	49.4	1151	2	Q41924_GIBZE	Q41924 gibberella	532	38	48.1	331	1	SHOX2_MOUSE	O6tgcx3 brachydanio
460	39	49.4	1222	2	Q55518_DICDI	Q55518 dictyosteli	533	38	48.1	331	1	SHOX2_MOUSE	O6tgcx3 brachydanio
461	39	49.4	1222	2	Q86SA4_DICDI	Q86sa4 dictyosteli	534	38	48.1	331	1	SHOX2_MOUSE	O6tgcx3 brachydanio
462	39	49.4	1222	2	Q86SA4_DICDI	Q86sa4 dictyosteli	535	38	48.1	331	1	SHOX2_MOUSE	O6tgcx3 brachydanio
463	38.5	48.7	1083	2	O45935_CABEL	O45935 caenorhabdi	536	38	48.1	331	1	SHOX2_MOUSE	O6tgcx3 brachydanio
464	38.5	48.7	1150	2	Q624G9_CABER	Q624g9 caenorhabdi	537	38	48.1	331	1	SHOX2_MOUSE	O6tgcx3 brachydanio
465	38	48.1	82	2	Q5TY01_ANOGA	Q5ty01 anopheles p	538	38	48.1	331	1	SHOX2_MOUSE	O6tgcx3 brachydanio
466	38	48.1	92	2	O4JH20_ICTPU	O4jhz0 ictalurus p	539	38	48.1	331	1	SHOX2_MOUSE	O6tgcx3 brachydanio
467	38	48.1	144	2	Q8QSK0_FUGRU	Q8qsk0 fugu rubrip	540	38	48.1	331	1	SHOX2_MOUSE	O6tgcx3 brachydanio
468	38	48.1	146	2	Q72XD4_BACCI	Q72xd4 bacillus ce	541	38	48.1	331	1	SHOX2_MOUSE	O6tgcx3 brachydanio
469	38	48.1	158	2	Q9AVD8_TOBAC	Q9avd8 nicotiana t	542	38	48.1	331	1	SHOX2_MOUSE	O6tgcx3 brachydanio

543	38	48.1	753	2	Q5X2A6_LEGPA	Q5x2a6	legionella	616	37	45.8	541	2	Q7VAL17_PROMA	Q7val17	prochloroco
544	38	48.1	753	2	Q5ZSU4_LESGPH	Q5zsu4	legionella	617	37	45.8	552	2	Q4QCZ0_LEIMA	Q4qcz0	leishmania
545	38	48.1	777	2	Q7QSE9_GIALA	Q7qse9	giardia lam	618	37	45.8	555	2	Q6RFT1_APIME	Q6rft1	apis mellif
546	38	48.1	803	2	Q583A3_9TRYP	Q583a3	trypanosoma	619	37	45.8	556	2	Q5C8T4_PETHY	Q5c8t4	petunia hyb
547	38	48.1	838	1	CEP1_CRYNE	Q5k9l1	cryptococcu	620	37	45.8	556	2	Q5IF11_PETHY	Q5if11	petunia hyb
548	38	48.1	873	1	ZHX1_HUMAN	Q9kyv1	homo sapien	621	37	45.8	563	2	Q6C9W8_YARLI	Q6c9w8	yarrowia li
549	38	48.1	873	1	ZHX1_MOUSE	P70121	mus musculu	622	37	45.8	574	2	Q960E9_DROME	Q960e9	drosophila
550	38	48.1	873	1	ZHX1_RAT	Q8r515	rattus norv	623	37	45.8	575	2	Q8LGJ2_ARATH	Q8lgj2	arabidopsis
551	38	48.1	888	1	ETOL1_ARATH	Q92qx6	arabidopsis	624	37	45.8	575	2	Q9LZM8_ARATH	Q9lzm8	arabidopsis
552	38	48.1	906	2	Q5DTL2_MOUSE	Q5dtl2	mus musculu	625	37	45.8	575	2	Q8HL47_ARATH	Q8hl47	arabidopsis
553	38	48.1	915	2	Q6GR48_XENLA	Q6gr48	xenopus lae	626	37	45.8	580	2	Q4RQ19_TETNG	Q4rq19	tetraodon n
554	38	48.1	916	2	Q6DEH6_BRARE	Q6deh6	brachydanio	627	37	45.8	586	2	Q5PLH3_SALPA	Q5plh3	salmonella
555	38	48.1	922	2	Q93XG0_MAIZE	Q93xg0	zea mays (m	628	37	45.8	596	2	Q7CP97_SALTY	Q7cp97	salmonella
556	38	48.1	1006	1	K125_TOBAC	Q23826	nicotiana t	629	37	45.8	596	2	Q8F5L5_SALTI	Q8f5l5	salmonella
557	38	48.1	1032	2	Q80491_ARATH	Q80491	arabidopsis	630	37	45.8	601	1	FRDA_ECOLI	P00363	escherichia
558	38	48.1	1040	2	Q8A203_BACTN	Q8a203	bacteroides	631	37	45.8	602	2	Q83P37_SHIFL	Q83p37	shigella fl
559	38	48.1	1045	2	Q94G20_DAUCA	Q94g20	daucus caro	632	37	45.8	602	2	Q8FAL6_ECOL6	Q8fal6	escherichia
560	38	48.1	1056	2	Q5W7C6_ORYSA	Q5w7c6	oryza sativ	633	37	45.8	602	2	Q8XDQ0_ECO57	Q8xdq0	escherichia
561	38	48.1	1058	2	Q9S0U0_ARATH	Q9s0u0	arabidopsis	634	37	45.8	603	2	Q889P6_ORYLA	Q889p6	oryzias lat
562	38	48.1	1058	2	Q9LZU5_ARATH	Q9lzu5	arabidopsis	635	37	45.8	603	2	Q8UUL1_ORYLA	Q8uul1	oryzias lat
563	38	48.1	1076	2	Q9S1B3_ARATH	Q9s1b3	arabidopsis	636	37	45.8	624	2	Q57GN4_SALCH	Q57gn4	salmonella
564	38	48.1	1087	2	Q8G292_GIBMO	Q8g292	gibberella	637	37	45.8	628	2	Q585N4_9TRYP	Q585n4	trypanosoma
565	38	48.1	1248	2	Q6P9P4_BRARE	Q6p9p4	brachydanio	638	37	45.8	643	1	CTK2_XENLA	P79955	xenopus lae
566	38	48.1	1265	2	Q6RZ29_DICDI	Q6rzz9	dictyosteli	639	37	45.8	643	1	Q5XGK6_XENLA	Q5xgk6	xenopus lae
567	38	48.1	1300	1	ATG11_NEUCR	Q78055	neurospora	640	37	45.8	668	2	Q8CON1_MOUSE	Q8con1	mus musculu
568	38	48.1	1304	2	Q9SUK4_ARATH	Q9suk4	arabidopsis	641	37	45.8	675	2	Q5XGB8_XENTR	Q5xgb8	xenopus tro
569	38	48.1	1310	2	Q4RM26_TETNG	Q4rm26	tetraodon n	642	37	45.8	708	2	Q4SZU6_TETNG	Q4szu6	tetraodon n
570	38	48.1	1385	2	Q7TSP2_RAT	Q7tsp2	rattus norv	643	37	45.8	709	2	Q74ZE6_ASHGO	Q74ze6	ashbya goss
571	38	48.1	1385	2	Q7TN17_RAT	Q7tn17	rattus norv	644	37	45.8	722	2	Q54IG2_DICDI	Q54ig2	dictyosteli
572	38	48.1	1386	2	Q984C1_RHILO	Q984c1	rhizobium l	645	37	45.8	727	2	Q54UT1_DICDI	Q54ut1	dictyosteli
573	38	48.1	1387	2	Q70MX5_MOUSE	Q70mx5	mus musculu	646	37	45.8	729	2	Q81HF4_DROME	Q81hf4	drosophila
574	38	48.1	1387	2	Q6P9L6_MOUSE	Q6p9l6	mus musculu	647	37	45.8	729	2	Q9W1U1_DROME	Q9w1u1	drosophila
575	38	48.1	1388	2	Q9NS87_HUMAN	Q9ns87	homo sapien	648	37	45.8	800	2	P92163_STRPU	P92163	strongyloce
576	38	48.1	1388	2	Q91S78_XENLA	Q91s78	xenopus lae	649	37	45.8	803	2	Q7RT59_PLAYO	Q7rt59	plasmaodium
577	38	48.1	1793	2	Q4HXW9_GIBZE	Q4hwx9	gibberella	650	37	45.8	810	1	ZN33A_HUMAN	Q06730	homo sapien
578	38	48.1	1873	2	Q6S0Q3_DICDI	Q6s0q3	dictyosteli	651	37	45.8	810	1	Q5VZ86_HUMAN	Q5vz86	homo sapien
579	38	48.1	1874	2	Q6LSQ4_CAEBR	Q6lsq4	caenorhabdi	652	37	45.8	839	2	Q94HCL_ORYSA	Q94hcl	oryza sativ
580	38	48.1	2121	2	Q4QC92_LEIMA	Q4qc92	leishmania	653	37	45.8	839	2	Q7XF10_ORYSA	Q7xf10	oryza sativ
581	37.5	47.5	465	2	Q4R302_MACFA	Q4rc92	macaca fasc	654	37	45.8	841	2	Q5W6W1_ORYSA	Q5w6w1	oryza sativ
582	37	46.8	90	2	Q7JNH7_STRPU	Q7jnh7	strongyloce	655	37	45.8	844	2	Q6BT18_DBBHA	Q6bt18	debaromyce
583	37	46.8	153	2	Q9NFA2_PLAF7	Q9nfa2	plasmaodium	656	37	45.8	859	2	Q8JDJ1_9HIV1	Q8jdj1	human immun
584	37	46.8	159	1	IGJ_MOUSE	P01592	mus musculu	657	37	45.8	862	2	Q6H535_ORYSA	Q6h535	oryza sativ
585	37	46.8	159	2	Q4QQV9_RAT	Q4qqv9	rattus norv	658	37	45.8	864	2	Q5KCB8_CRYNE	Q5kcb8	cryptococcu
586	37	46.8	167	2	Q9AVD3_TOBAC	Q9avd3	nicotiana t	659	37	45.8	865	2	Q6JWU2_9BACT	Q6jwu2	uncultured
587	37	46.8	176	2	Q89VY0_BRAJA	Q89vy0	bradyrhizob	660	37	45.8	872	2	Q9YZ97_9VIRU	Q9yz97	navel orang
588	37	46.8	178	2	Q59ZR8_CANAL	Q59zr8	candida alb	661	37	45.8	884	2	Q5U4X1_XENLA	Q5u4x1	xenopus lae
589	37	46.8	188	2	Q23604_CAEEL	Q23604	caenorhabdi	662	37	45.8	887	2	Q6DEA8_XENLA	Q6dea8	xenopus lae
590	37	46.8	190	2	Q6AH83_LEIXX	Q6ah83	leifsonia x	663	37	45.8	890	1	K120A_HUMAN	Q95235	homo sapien
591	37	46.8	226	2	Q59UUS_CANAL	Q59ju5	candida alb	664	37	45.8	890	2	Q8W5R6_ARATH	Q8w5r6	arabidopsis
592	37	46.8	233	2	Q4RE76_TETNG	Q4re76	tetraodon n	665	37	45.8	899	2	P74477_SYNY3	P74477	synecocyst
593	37	46.8	237	2	Q41PU7_GIBZE	Q41pu7	gibberella	666	37	45.8	909	2	Q9X103_ARATH	Q9x103	arabidopsis
594	37	46.8	253	2	Q632R6_BACCZ	Q632r6	bacillus ce	667	37	45.8	924	2	Q7ZWT5_XENLA	Q7zwt5	xenopus lae
595	37	46.8	255	2	Q8A6G0_BACTN	Q8a6g0	bacteroides	668	37	45.8	929	2	Q5VWA9_HUMAN	Q5vwa9	homo sapien
596	37	46.8	290	2	Q8TYK4_METKA	Q8tyk4	mechanopyru	669	37	45.8	933	2	Q88F05_XENLA	Q88f05	xenopus lae
597	37	46.8	292	2	Q602L2_METCA	Q602l2	methylococc	670	37	45.8	938	2	Q7SDI4_NEUCR	Q7sdi4	neurospora
598	37	46.8	304	2	Q5AH08_CANAL	Q5ah08	candida alb	671	37	45.8	944	2	Q5XGE8_XENTR	Q5xge8	xenopus tro
599	37	46.8	308	2	Q612G6_CAEBR	Q612g6	caenorhabdi	672	37	45.8	960	2	Q23404_ARATH	Q23404	arabidopsis
600	37	46.8	329	1	Y135_MYCPN	P75263	mycoplasma	673	37	45.8	963	2	Q5SJE1_CRYNE	Q5sje1	cryptococcu
601	37	46.8	374	2	Q5F3M7_CHICK	Q5f3m7	gallus gall	674	37	45.8	1016	2	Q6QIV7_XENNE	Q6qiv7	xenorhabdu
602	37	46.8	404	2	Q7PTN3_ANOGA	Q7ptn3	anopheles g	675	37	45.8	1018	2	Q8MWC_GOSHI	Q8mwc6	gossypium h
603	37	46.8	404	2	Q5TXC8_ANOGA	Q5txc8	anopheles g	676	37	45.8	1027	2	Q8A549_BACTN	Q8a549	bacteroides
604	37	46.8	420	2	Q8SRB7_ENCCU	Q8srb7	encephalito	677	37	45.8	1028	2	Q6GSA8_HUMAN	Q6gsa8	homo sapien
605	37	46.8	445	2	Q5NA73_ORYSA	Q5na73	oryza sativ	678	37	45.8	1029	1	KIF17_HUMAN	Q9p2e2	homo sapien
606	37	46.8	449	2	Q6SDH7_BACLD	Q6sdh7	bacillus li	679	37	45.8	1029	2	Q53Y86_HUMAN	Q53y86	homo sapien
607	37	46.8	465	1	LIF10_CANAL	Q9p4e5	candida alb	680	37	45.8	1055	2	Q8RW44_ARATH	Q8rwa4	arabidopsis
608	37	46.8	465	2	Q5APE3_CANAL	Q5ape3	candida alb	681	37	45.8	1055	2	Q8W5R5_ARATH	Q8w5r5	arabidopsis
609	37	46.8	469	2	Q6UNX5_NICBE	Q6unx5	nicotiana b	682	37	45.8	1056	1	K125_ARATH	P82266	arabidopsis
610	37	46.8	496	2	Q5L378_GEOKA	Q5l378	geobacillus	683	37	45.8	1068	2	Q9VNC7_DROME	Q9vnc7	drosophila
611	37	46.8	507	2	Q52024_HALSA	Q52024	halobacteri	684	37	45.8	1116	2	Q5FAM3_BRAOL	Q5fam3	brassica ol
612	37	46.8	512	2	Q528B5_MAGGR	Q528b5	magnaporthe	685	37	45.8	1121	2	Q9SVI8_ARATH	Q9svi8	arabidopsis
613	37	46.8	513	2	Q6Z488_ORYSA	Q6z488	oryza sativ	686	37	45.8	1162	2	Q9LPQ7_ARATH	Q9lpq7	arabidopsis
614	37	46.8	538	2	Q59VZ1_CANAL	Q59vz1	candida alb	687	37	45.8	1188	2	Q9SE56_DROME	Q9se56	drosophila
615	37	46.8	539	2	Q82FQ5_STRAW	Q82fq5	streptomyce	688	37	45.8	1195	2	Q9C7T0_ARATH	Q9c7t0	arabidopsis

689	37	46.8	1196	2	Q7RL15_PLAYO	Q7rl15 plasmodium	762	36	45.6	313	2	Q9ZRU3_CICAR	Q9zru3 cicar ariet
690	37	46.8	1212	2	Q4Q7F9_LEIMA	Q4q7f9 leishmania	763	36	45.6	322	1	Q4QXK1_HAE18	Q4qkx1 haemophilus
691	37	46.8	1215	2	Q7KTI7_DROME	Q7kti7 drosophila	764	36	45.6	323	1	MRAW_GLUOX	Q5fuk3 gluconobact
692	37	46.8	1274	1	ARMI_DROME	Q615k9 drosophila	765	36	45.6	326	2	Q6BGJ6 PARTE	Q6bgj6 paramesich
693	37	46.8	1361	2	Q04264_ARATH	Q04264 arabidopsis	766	36	45.6	326	2	Q8FKS0_ECOL6	Q8fks0 escherichia
694	37	46.8	1437	2	Q5JN29_ORYSA	Q5jnz9 oryza sativ	767	36	45.6	330	1	RS2_MYCPU	Q98q36 mycoplasma
695	37	46.8	1461	2	Q8TF96_DROME	Q8tf96 drosophila	768	36	45.6	333	2	Q4LJE1_9EURK	Q4lje1 burkholderi
696	37	46.8	1463	2	Q9GY20_STRPU	Q9gy20 strongyloce	769	36	45.6	344	2	Q61754_CABEL	Q61754 caenorhabdi
697	37	46.8	1474	2	Q8T4M0_DROME	Q8t4m0 drosophila	770	36	45.6	356	2	Q54JY7_DICDI	Q54jy7 dictyosteli
698	37	46.8	1503	2	Q874L8_DROME	Q874l8 drosophila	771	36	45.6	359	2	Q51206_NEISER	Q51206 neisseria m
699	37	46.8	1503	2	Q7KTI8_DROME	Q7kti8 drosophila	772	36	45.6	373	2	Q6GND5_XENLA	Q6gnd5 xenopus lae
700	37	46.8	1506	2	Q4N7X6_THEPA	Q4n7x6 theileria p	773	36	45.6	374	2	Q6ZNL1_HUMAN	Q6znl1 homo sapien
701	37	46.8	1509	2	Q9SP10_DROME	Q9sp10 drosophila	774	36	45.6	375	2	P93066_BRANA	P93066 brassica na
702	37	46.8	1509	2	Q5VLQ8_DROME	Q5vlg8 drosophila	775	36	45.6	384	1	HEP1_PEDHE	Q5819 pedobacter
703	37	46.8	1509	2	Q81PG1_DROME	Q81pg1 drosophila	776	36	45.6	385	2	Q7BQX3_9ENTR	Q7bqx3 serratia en
704	37	46.8	1605	2	Q17887_CABEL	Q17887 caenorhabdi	777	36	45.6	388	2	Q9X6U4_NEIME	Q9x6u4 neisseria m
705	37	46.8	1609	2	Q9GRC3_CABEL	Q9grc3 caenorhabdi	778	36	45.6	396	2	Q8UG5_LACPL	Q8ug5 lactobacill
706	37	46.8	1619	2	Q77382_PLAUF	Q77382 plasmodium	779	36	45.6	401	2	Q8CBV4_MYCLE	Q8cbv4 mycobacteri
707	37	46.8	1641	2	Q5LJZ2_DROME	Q5ljz2 drosophila	780	36	45.6	408	2	Q9GHK2_9SOLA	Q9ghk2 lycium afri
708	37	46.8	1843	2	Q5JLC8_ORYSA	Q5jlc8 oryza sativ	781	36	45.6	411	1	MSK2_MEDSA	P51138 medicago sa
709	37	46.8	2158	2	Q9LUT5_ARATH	Q9lut5 arabidopsis	782	36	45.6	421	2	Q9W5Q1_DROME	Q9w5q1 drosophila
710	37	46.8	2391	2	Q5D862_HUMAN	Q5d862 homo sapien	783	36	45.6	421	2	Q81NC2_BACAN	Q81nc2 bacillus an
711	37	46.8	2523	2	Q9VTP0_DROME	Q9vtp0 drosophila	784	36	45.6	422	2	Q6AIW9_DESPS	Q6aiw9 desulfotale
712	36	45.6	72	2	Q8Y0W3_RALSO	Q8y0w3 ralstonia s	785	36	45.6	436	2	Q7S185_NEUCR	Q7s185 neurospora
713	36	45.6	77	2	Q82PE4_STRAW	Q82pe4 streptomyce	786	36	45.6	445	2	Q63US9_BURPS	Q63us9 burkholderi
714	36	45.6	82	2	Q5TSJ6_ANOGA	Q5tsej6 anopheles g	787	36	45.6	447	1	Y418_HATIN	Q41k84 gibberella
715	36	45.6	83	2	Q4TE09_TETNG	Q4te09 tetraodon n	788	36	45.6	453	2	Q4IK84_GIBZE	Q4ik84 gibberella
716	36	45.6	101	2	Q68775_YERPE	Q68775 yersinia pe	789	36	45.6	453	2	Q4HN01_CAMLA	Q4hn01 campylobact
717	36	45.6	101	2	Q68775_YERPE	Q68775 yersinia pe	790	36	45.6	460	2	Q62JW8_BURMA	Q62jw8 burkholderi
718	36	45.6	101	2	Q935D1_SALTI	Q935d1 salmonella	791	36	45.6	468	2	Q5JN15_ORYSA	Q5jnl5 oryza sativ
719	36	45.6	139	2	Q51610_9ZZZZ	Q51610 plasmid col	792	36	45.6	479	2	Q7T318_BRARE	Q7t318 brachydanio
720	36	45.6	139	2	Q51625_9ZZZZ	Q51625 plasmid col	793	36	45.6	482	2	Q5J4W3_FUGRU	Q5j4w3 fugu rubrip
721	36	45.6	152	2	Q5J8X5_HUMAN	Q5j8x5 homo sapien	794	36	45.6	486	2	Q96700_9CAEN	Q96700 illyanassa o
722	36	45.6	159	2	Q35057_MOUSE	Q35057 mus musculu	795	36	45.6	494	2	Q4P3K0_USTWA	Q4p3k0 ustilago ma
723	36	45.6	160	2	Q35063_MOUSE	Q35063 mus musculu	796	36	45.6	494	2	Q5L7S9_BACFN	Q5l7s9 bacteroides
724	36	45.6	163	2	Q54719_RAT	Q54719 rattus norv	797	36	45.6	505	2	Q5V1P6_HALMA	Q5v1p6 halorcula
725	36	45.6	166	2	Q8R7A3_THETN	Q8r7a3 thermoanaer	798	36	45.6	512	2	Q9H6Q9_HUMAN	Q9h6q9 homo sapien
726	36	45.6	168	2	Q79N46_LACLC	Q79n46 lactococcus	799	36	45.6	513	2	Q47919_FISSU	Q47919 fischerella
727	36	45.6	174	2	Q4IMX3_GIBZE	Q4imx3 gibberella	800	36	45.6	513	2	Q8YKT1_ANASP	Q8ykt1 anabaena sp
728	36	45.6	174	2	Q717T1_MOUSE	Q717t1 mus musculu	801	36	45.6	515	2	Q4SEA0_TETNG	Q4sea0 tetraodon n
729	36	45.6	179	2	Q9MCV1_BPHKO	Q9mcv1 bacterioph	802	36	45.6	538	2	Q7UHD3_RHOBA	Q7uhd3 rhodopirall
730	36	45.6	182	1	LEP_BACCL	P41027 bacillus ca	803	36	45.6	555	2	Q8D625_VIBVU	Q8d625 vibrio vuln
731	36	45.6	182	2	Q5L265_GEOKA	Q5l265 geobacillus	804	36	45.6	564	2	Q54UR1_DICDI	Q54uri dictyosteli
732	36	45.6	197	2	Q7VGK9_HELHP	Q7vgk9 helicobacte	805	36	45.6	565	2	Q5KMD1_CRYNE	Q5kmd1 cryptococcu
733	36	45.6	198	1	SCPB_STRMU	Q7zak9 streptococc	806	36	45.6	566	2	Q7KZ68_HUMAN	Q7kz68 homo sapien
734	36	45.6	199	2	Q8UJ2T_AGR75	Q8uju2 agrobacteri	807	36	45.6	571	2	Q7MD48_VIBVU	Q7md48 vibrio vuln
735	36	45.6	202	2	Q9XUW8_CABEL	Q9xu8 caenorhabdi	808	36	45.6	582	2	Q5CKC7_CRYHO	Q5ckc7 cryptospori
736	36	45.6	203	2	Q5FWC3_MOUSE	Q5fwc3 mus musculu	809	36	45.6	583	2	Q5CR50_CRYPV	Q5cr50 cryptospori
737	36	45.6	204	2	Q927S3_LISIN	Q927s3 listeria in	810	36	45.6	583	2	Q9KLR7_VIBCH	Q9klr7 vibrio chol
738	36	45.6	204	2	Q71WK8_LISMF	Q71wk8 listeria mo	811	36	45.6	586	2	Q7Q4J4_ANOGA	Q7q4j4 anopheles g
739	36	45.6	204	2	Q8Y485_LISMO	Q8y485 listeria mo	812	36	45.6	587	2	Q6Z3Z9_ORYSA	Q6z3z9 oryza sativ
740	36	45.6	204	2	Q8QNN3_9PHYC	Q8qnn3 ectocarpus	813	36	45.6	594	2	Q55XK3_CRYNE	Q55xk3 cryptococcu
741	36	45.6	214	2	Q48637_9LACT	Q48637 lactococcus	814	36	45.6	598	2	Q4V1B4_BACCZ	Q4vlb4 bacillus ce
742	36	45.6	229	2	Q6R023_CABEL	Q6r023 caenorhabdi	815	36	45.6	598	2	Q6D032_ERWCT	Q6d032 erwinia car
743	36	45.6	232	2	Q5FBG4_9HYPO	Q5fbg4 fusarium sp	816	36	45.6	610	2	Q32582_ECOLI	Q32582 escherichia
744	36	45.6	238	2	Q5JN14_ORYSA	Q5jni14 oryza sativ	817	36	45.6	613	2	Q93LN4_XANCV	Q93ln4 xanthomonas
745	36	45.6	246	2	Q30519_MYCSM	Q30519 mycobacteri	818	36	45.6	622	2	Q4V9Q4_BRARE	Q4v9q4 brachydanio
746	36	45.6	248	2	Q7D7I3_MYCTU	Q7d7i3 mycobacteri	819	36	45.6	631	2	Q60443_CRIGR	Q60443 cricetulus
747	36	45.6	248	2	Q7TZ14_MYCTU	Q7tz14 mycobacteri	820	36	45.6	626	1	X159C_DROME	Q9xlu4 drosophila
748	36	45.6	248	2	Q33244_MYCTU	Q33244 mycobacteri	821	36	45.6	628	2	Q5SM09_CRYNE	Q5sm09 cryptococcu
749	36	45.6	255	2	Q9AKN6_RICMO	Q9akn6 rickettsia	822	36	45.6	628	2	Q5K8R0_CRYNE	Q5k8r0 cryptococcu
750	36	45.6	256	2	Q82GA8_STRAW	Q82ga8 streptomyce	823	36	45.6	631	2	Q60SW1_CAEBR	Q60sw1 caenorhabdi
751	36	45.6	262	2	Q82H10_STRAW	Q82h10 streptomyce	824	36	45.6	666	2	Q4QR27_XENLA	Q4qr27 xenopus lae
752	36	45.6	263	2	Q4HEA9_CAMCO	Q4hea9 campylobact	825	36	45.6	673	1	K1FC1_HUMAN	Q5su09 homo sapien
753	36	45.6	265	2	Q49792_MYCLE	Q49792 mycobacteri	826	36	45.6	673	2	Q5SU09_HUMAN	Q5su09 homo sapien
754	36	45.6	265	2	Q9S375_MYCLE	Q9s375 mycobacteri	827	36	45.6	693	2	Q5X163_RAT	Q5xi63 rattus norv
755	36	45.6	269	2	Q6PC56_BRARE	Q6pc56 brachydanio	828	36	45.6	695	2	Q9Z4I4_NEIME	Q9z4i4 neisseria m
756	36	45.6	286	2	Q5L243_GEOKA	Q5l243 geobacillus	829	36	45.6	696	2	Q9H755_HUMAN	Q9h755 homo sapien
757	36	45.6	289	2	Q63A97_BURKHO	Q63a97 burkholderi	830	36	45.6	702	2	Q5ARZ0_EMENI	Q5arz0 aspergillus
758	36	45.6	299	2	Q62LS8_BURMA	Q62ls8 burkholderi	831	36	45.6	702	2	Q7YYK0_CRYPV	Q7yyk0 cryptospori
759	36	45.6	300	1	MRAW_CHLTR	Q62188 burkholderi	832	36	45.6	709	2	Q6P4A5_HUMAN	Q6p4a5 homo sapien
760	36	45.6	311	1	MRAW_PORGI	Q84274 chlamydia t	833	36	45.6	714	2	Q15718_DICDI	Q15718 dictyosteli
761	36	45.6	311	1	MRAW_PORGI	Q87mn0 porphyromon	834	36	45.6	714	2	Q5CU31_CRYHO	Q5cuj31 cryptospori

835	36	45.6	715	2	Q9US53_SCHPO	Q9ue53 schizosacch	908	36	45.6	1743	2	Q9XWX5_CABEL	Q9xwx5 caenorhabdi
836	36	45.6	719	2	Q4KMP0_HUMAN	Q4kmp0 homo sapien	909	36	45.6	1748	2	Q61TP1_CAEBR	Q61tp1 mus musculus
837	36	45.6	720	2	Q6GMS7_HUMAN	Q6gms7 homo sapien	910	36	45.6	1749	1	X113A_MOUSE	Q9eqw7 mus musculus
838	36	45.6	730	2	Q86Z96_GIBMO	Q86z96 gibberella	911	36	45.6	1749	2	Q9H193_HUMAN	Q9h193 homo sapien
839	36	45.6	743	2	Q5R7M5_PONPY	Q5r7m5 pongo pygma	912	36	45.6	1752	2	Q9H194_HUMAN	Q9h194 homo sapien
840	36	45.6	753	2	Q09471_HUMAN	Q09471 homo sapien	913	36	45.6	1767	2	Q70AM4_RAT	Q70am4 rattus norv
841	36	45.6	762	2	Q7YV00_9TRYP	Q7yv00 trypanosoma	914	36	45.6	1768	2	Q5THQ2_HUMAN	Q5thq2 homo sapien
842	36	45.6	780	2	Q6P0K1_BRARE	Q6p0k1 brachydanio	915	36	45.6	1780	2	Q5T9M3_HUMAN	Q5t9m3 homo sapien
843	36	45.6	783	2	Q5U4W5_XENLA	Q5u4w5 xenopus lae	916	36	45.6	1780	2	Q9UFR5_HUMAN	Q9ufr5 homo sapien
844	36	45.6	789	2	Q61BQ0_CAEBR	Q61bq0 caenorhabdi	917	36	45.6	1798	2	Q4S8D9_TETNG	Q4s8d9 tetraodon n
845	36	45.6	789	2	Q9SP24_CABEL	Q9sp24 caenorhabdi	918	36	45.6	1803	2	Q5THQ3_HUMAN	Q5thq3 homo sapien
846	36	45.6	791	2	Q7112J1_RAT	Q7112j1 rattus norv	919	36	45.6	1805	1	K113A_HUMAN	Q9h1h9 homo sapien
847	36	45.6	792	1	K1FC2_MOUSE	Q08672 mus musculu	920	36	45.6	1820	2	Q96Q89_HUMAN	Q96q89 homo sapien
848	36	45.6	792	2	Q9BP03_DICDI	Q9bp03 dictyosteli	921	36	45.6	1820	2	Q5T9N0_HUMAN	Q5t9n0 homo sapien
849	36	45.6	805	1	K110A_DROME	Q96020 drosophila	922	36	45.6	1826	1	K113B_HUMAN	Q9h1h9 homo sapien
850	36	45.6	808	2	Q5Z155_CHICK	Q5z155 gallus gall	923	36	45.6	1830	2	Q4P9C7_USTMA	Q4p9c7 ustilago ma
851	36	45.6	820	2	Q4SFK9_TETNG	Q4sfk9 tetraodon n	924	36	45.6	1867	2	Q4R101_TETNG	Q4r101 tetraodon n
852	36	45.6	829	1	SPD2_CAEBR	Q61dp2 caenorhabdi	925	36	45.6	1982	2	Q4SFX7_TETNG	Q4sfx7 tetraodon n
853	36	45.6	829	2	Q6FV25_CANGA	Q6fv25 candida gla	926	36	45.6	2262	2	Q4RF46_TETNG	Q4rf46 tetraodon n
854	36	45.6	840	2	Q4G6N4_LEIMA	Q4g6n4 leishmania	927	36	45.6	2335	2	Q6PM77_9PICO	Q6pmt7 foot-and-mo
855	36	45.6	859	2	Q9FW70_ORYSA	Q9fw70 oryza sativ	928	36	45.6	2335	2	Q9Q2N9_9PICO	Q9q2n9 foot-and-mo
856	36	45.6	864	2	Q5QL86_ORYSA	Q5ql86 oryza sativ	929	36	45.6	2340	2	Q6PMU2_9PICO	Q6pmu2 foot-and-mo
857	36	45.6	867	2	Q7ZU15_BRARE	Q7zu15 brachydanio	930	35.5	44.9	107	2	Q4T0X3_TETNG	Q4t0x3 tetraodon n
858	36	45.6	867	2	Q9PUU5_BRARE	Q9puu5 brachydanio	931	35.5	44.9	294	2	Q8L619_ARATH	Q8l619 arabidopsis
859	36	45.6	871	2	Q5XGE1_XENTR	Q5xge1 xenopus tro	932	35.5	44.9	294	2	Q9SY11_ARATH	Q9sy11 arabidopsis
860	36	45.6	878	2	Q4SHJ9_TETNG	Q4shj9 tetraodon n	933	35.5	44.9	469	1	Y0B1_CABEL	Q02255 caenorhabdi
861	36	45.6	882	2	Q5CVF6_CRYPV	Q5cvf6 cryptospori	934	35.5	44.9	570	2	Q55XR3_CRYNE	Q55xr3 cryptococcu
862	36	45.6	882	2	Q5CHP4_CRYHO	Q5chp4 cryptospori	935	35.5	44.9	574	2	Q5KM77_CRYNE	Q5km77 cryptococcu
863	36	45.6	886	2	Q6W855_ORYSA	Q6w855 oryza sativ	936	35.5	44.9	574	2	Q9V4A1_DROME	Q9v4a1 drosophila
864	36	45.6	895	2	Q1LNA4_ARATH	Q1lna4 arabidopsis	937	35.5	44.9	649	2	Q6NNT2_DROME	Q6nnt2 drosophila
865	36	45.6	897	2	Q6DFB2_XENLA	Q6dfb2 xenopus lae	938	35.5	44.9	3004	2	Q4SN41_TETNG	Q4sn41 tetraodon n
866	36	45.6	904	2	Q6DBE5_ERWCT	Q6dbe5 erwinia car	939	35.5	44.9	3902	2	Q4SC60_TETNG	Q4sc60 tetraodon n
867	36	45.6	915	1	ATCU_VIBCH	Q9kpz7 vibrio chol	940	35	44.3	58	2	Q8D124_WIGBR	Q8d124 wigglewort
868	36	45.6	919	2	Q4WG65_ASPPU	Q4wg65 aspergillus	941	35	44.3	72	2	Q860T2_CHICK	Q860t2 gallus gall
869	36	45.6	919	2	Q9FZ06_ARATH	Q9fz06 arabidopsis	942	35	44.3	86	2	Q502C6_BRARE	Q502c6 brachydanio
870	36	45.6	927	2	Q4U8G8_THEAN	Q4u8g8 theileria a	943	35	44.3	87	1	VP08_BEAPS	Q9f1u0 bacterioph
871	36	45.6	939	2	Q41P54_GIBZE	Q41p54 gibberella	944	35	44.3	88	2	Q7QUG7_GIALA	Q7qug7 giardia lam
872	36	45.6	941	2	Q4N163_THEPA	Q4n163 theileria p	945	35	44.3	92	1	DBH_BUCAI	Q5gn10 oryza sativ
873	36	45.6	972	2	Q51UW9_MAGGR	Q51uw9 magnaporthe	946	35	44.3	98	2	Q5QN10_ORYSA	Q5qn10 oryza sativ
874	36	45.6	984	2	Q9U0K0_PLAUF7	Q9u0k0 plasmodium	947	35	44.3	95	2	Q6Z6N7_ORYSA	Q6z6n7 oryza sativ
875	36	45.6	1004	2	Q4WJ77_ASPPU	Q4wj77 aspergillus	948	35	44.3	101	2	Q9V977_9VIRU	Q9v977 hop mosaic
876	36	45.6	1014	2	Q93RN9_XENNE	Q93rn9 xenorhabdus	949	35	44.3	102	2	Q5RHI7_BRARE	Q5rhi7 brachydanio
877	36	45.6	1025	2	Q5R8P8_PONPY	Q5r8p8 pongo pygma	950	35	44.3	102	2	Q5SNV3_BRARE	Q5snv3 brachydanio
878	36	45.6	1038	1	K1F17_MOUSE	Q99pw8 mus musculu	951	35	44.3	104	2	Q502B5_BRARE	Q502es brachydanio
879	36	45.6	1087	2	Q6SA74_9VIRU	Q6sa74 cherry chlo	952	35	44.3	121	2	Q9Z4H2_STRCO	Q9z4h2 streptomyce
880	36	45.6	1087	2	Q65A77_9VIRU	Q65a77 amasya cher	953	35	44.3	122	2	Q5I314_ECOLI	Q5i314 escherichia
881	36	45.6	1116	2	Q7Z5E0_HUMAN	Q7z5e0 homo sapien	954	35	44.3	124	2	Q9F3Z7_NEIME	Q9f3z7 neisseria m
882	36	45.6	1175	2	Q13632_HUMAN	Q13632 homo sapien	955	35	44.3	126	2	Q6GBQ5_STAAS	Q6gbq5 staphylococ
883	36	45.6	1184	2	Q7Y1L9_CRYPV	Q7y1l9 cryptospori	956	35	44.3	126	2	Q5H194_STAAC	Q5h194 staphylococ
884	36	45.6	1184	2	Q5CH49_CRYHO	Q5ch49 cryptospori	957	35	44.3	126	2	Q7A764_STAAN	Q7a7w7 staphylococ
885	36	45.6	1193	2	Q7X7H8_ORYSA	Q7x7h8 oryza sativ	958	35	44.3	126	2	Q9W29_9TAAM	Q9w29 staphylococ
886	36	45.6	1206	2	Q9NTC1_HUMAN	Q9ntc1 homo sapien	959	35	44.3	126	2	Q9W29_9TAAM	Q9w29 staphylococ
887	36	45.6	1219	2	Q85W55_HUMAN	Q85w55 homo sapien	960	35	44.3	129	2	Q9PA02_XYLFA	Q9pa02 xyella fas
888	36	45.6	1236	2	Q54WQ2_DICDI	Q54wq2 dictyosteli	961	35	44.3	129	2	Q5MXB1_9CLOS	Q5mxb1 mint vein b
889	36	45.6	1264	2	Q5A444_CANAL	Q5a444 candida alb	962	35	44.3	130	2	Q6YMA9_LITLI	Q6yma9 littorina l
890	36	45.6	1264	2	Q5A496_CANAL	Q5a496 candida alb	963	35	44.3	131	2	Q6YMA9_LITLI	Q6yma9 littorina l
891	36	45.6	1268	2	Q9LUG0_ARATH	Q9lugo arabidopsis	964	35	44.3	138	2	Q4TCF3_TETNG	Q4tcf3 tetraodon n
892	36	45.6	1289	2	Q4T042_TETNG	Q4t042 tetraodon n	965	35	44.3	147	2	Q58IT3_9ACTO	Q58it3 streptomyce
893	36	45.6	1292	2	Q9LDN0_ARATH	Q9ldn0 arabidopsis	966	35	44.3	150	2	Q95068_HUMAN	Q95068 homo sapien
894	36	45.6	1293	2	Q8H7Z2_ORYSA	Q8h7z2 oryza sativ	967	35	44.3	151	2	Q91116_MORSA	Q91116 morone saxa
895	36	45.6	1307	2	Q8GY37_ARATH	Q8gy37 arabidopsis	968	35	44.3	151	2	Q91112_MORSA	Q91112 morone saxa
896	36	45.6	1307	2	Q9S710_ARATH	Q9s710 arabidopsis	969	35	44.3	155	2	Q35230_MOUSE	Q35230 mus musculu
897	36	45.6	1313	2	Q81Y78_ARATH	Q81y78 arabidopsis	970	35	44.3	160	1	K1F1C_MOUSE	Q35071 mus musculu
898	36	45.6	1371	2	Q51XB4_MAGGR	Q51xb4 magnaporthe	971	35	44.3	162	2	Q9W3Y0_DROME	Q9w3y0 drosophila
899	36	45.6	1373	2	Q81WES_HUMAN	Q81we9 homo sapien	972	35	44.3	165	2	Q8FBY3_ECLOS	Q8fby3 escherichia
900	36	45.6	1396	1	ATG26_EMENT	Q5b4c9 emericeila	973	35	44.3	167	2	Q9AVD4_TOBAC	Q9avd4 nicotiana t
901	36	45.6	1427	2	Q14207_HUMAN	Q14207 homo sapien	974	35	44.3	168	1	DYR_LACLA	Q59487 lactococcu
902	36	45.6	1427	2	Q16580_HUMAN	Q16580 homo sapien	975	35	44.3	172	2	Q6VU59_CHICK	Q6vu59 gallus gall
903	36	45.6	1479	2	Q4RIU7_TETNG	Q4riu7 tetraodon n	976	35	44.3	172	2	Q6VU62_CHICK	Q6vu62 gallus gall
904	36	45.6	1493	2	Q7PXF9_ANGA	Q7pxf9 anopheles g	977	35	44.3	172	2	Q861N2_CHICK	Q861n2 gallus gall
905	36	45.6	1556	2	Q5KNG1_CRYNE	Q5kng1 cryptococcu	978	35	44.3	175	2	Q6AZH4_XENLA	Q6azh4 xenopus lae
906	36	45.6	1556	2	Q55Z46_CRYNE	Q55z46 cryptococcu	979	35	44.3	179	2	Q6JGT4_CHICK	Q6jgt4 gallus gall
907	36	45.6	1662	2	Q23274_ARATH	Q23274 arabidopsis	980	35	44.3	179	2	Q6JGT8_CHICK	Q6jgt8 gallus gall

981 35 44.3 179 2 Q6JGU6 CHICK Q6JGU6 gallus gall
 982 35 44.3 179 2 Q6JGV1 CHICK Q6JGV1 gallus gall
 983 35 44.3 180 2 Q9GIT3 CHICK Q9GIT3 gallus gall
 984 35 44.3 180 2 Q9GIT5 CHICK Q9GIT5 gallus gall
 985 35 44.3 180 2 Q9GIT7 CHICK Q9GIT7 gallus gall
 986 35 44.3 181 2 Q4NBE1 CHICK Q4NBE1 arthrobacte
 987 35 44.3 188 1 SCBP_LACLA Q5CG34 lactococcus
 988 35 44.3 193 2 Q5M1H9 STRT1 Q5M1H9 streptococc
 989 35 44.3 193 2 Q5M621 STRT2 Q5M621 streptococc
 990 35 44.3 207 2 Q6MAS5 PARUW Q6MAS5 parachlamyd
 991 35 44.3 209 2 Q5D8V3 SCHJA Q5D8V3 schistosoma
 992 35 44.3 215 1 TRAJ9_ECOLI Q00738 escherichia
 993 35 44.3 222 1 FLPA_THEVO Q979P2 thermoplasma
 994 35 44.3 232 2 O15103 HUMAN O15103 homo sapien
 995 35 44.3 232 2 Q98231 CHICK Q98231 gallus gall
 996 35 44.3 232 2 Q7YPM6 CHICK Q7YPM6 gallus gall
 997 35 44.3 232 2 Q7YPM7 CHICK Q7YPM7 gallus gall
 998 35 44.3 235 2 Q87A11_XYLFT Q87A11 xyella fas
 999 35 44.3 239 2 Q5WCK1 BACSK Q5WCK1 bacillus cl
 1000 35 44.3 252 2 Q8AVK2_XENLA Q8AVK2 xenopus lae

ALIGNMENTS

RESULT 1
 Q4LE75 HUMAN
 ID Q4LE75_HUMAN PRELIMINARY; PRT; 2585 AA.
 AC Q4LE75;
 DT 13-SEP-2005 (TREMBLrel. 31, Created)
 DT 13-SEP-2005 (TREMBLrel. 31, Last sequence update)
 DT 13-SEP-2005 (TREMBLrel. 31, Last annotation update)
 DE CENPE variant protein (Fragment).
 GN Name=CENPE variant protein;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
 OC Homo.
 OX NCBI_TaxID=9606;
 [1]
 RN NUCLEOTIDE SEQUENCE.
 RP Nakajima D., Saito K., Yamakawa H., Kikuno R.F., Nakayama M.,
 RA Ohara R., Okazaki N., Koga H., Nagase T., Ohara O.;
 RT "Preparation of a set of expression-ready clones of mammalian long
 RT cDNAs encoding large proteins by the ORF trap cloning method.";
 RL Submitted (MAR-2005) to the EMBL/GenBank/DBS databases.
 DR EMBL; AB209996; BAE06078.1; -; mRNA.
 FT NON_TER 1
 SQ SEQUENCE 2585 AA; 302325 MW; 00FC4B1B2F2C7899 CRC64;

Query Match 100.0%; Score 79; DB 2; Length 2585;
 Best Local Similarity 100.0%; Pred. No. 4e-05;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RHYGETKNQRRSSRS 15
 Db 194 RHYGETKNQRRSSRS 208
 |||||

RESULT 2
 CENPE HUMAN
 ID CENPE_HUMAN STANDARD; PRT; 2663 AA.
 AC Q02224;
 DT 01-JUL-1993 (Rel. 26, Created)
 DT 01-JUL-1993 (Rel. 26, Last sequence update)
 DT 13-SEP-2005 (Rel. 48, Last annotation update)
 DE Centromeric protein E (CENP-E protein).
 GN Name=CENPE;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
 OC Homo.
 OX NCBI_TaxID=9606;

RN NUCLEOTIDE SEQUENCE.
 RP MEDLINE=93024922; PubMed=1406971; DOI=10.1038/359536a0;
 RX Yen T.J., Li G., Schaar B.T., Szilak I., Cleveland D.W.;
 RA "CENP-E is a putative kinetochore motor that accumulates just before
 RT mitosis.";
 RL Nature 359:536-539 (1992).
 [2]
 RN CHARACTERIZATION.
 RP MEDLINE=95196755; PubMed=7889940;
 RX Thrower D.A., Jordan M.A., Schaar B.T., Yen T.J., Wilson L.;
 RA "Mitotic HeLa cells contain a CENP-E-associated minus end-directed
 RT microtubule motor.";
 RL EMBO J. 14:918-926 (1995).
 [3]
 RN CHARACTERIZATION.
 RP MEDLINE=98437347; PubMed=9763420; DOI=10.1083/jcb.143.1.49;
 RX Chan G.K.T., Schaar B.T., Yen T.J.;
 RA "Characterization of the kinetochore binding domain of CENP-E reveals
 RT interactions with the kinetochore proteins CENP-F and hBUBR1.";
 RL J. Cell Biol. 143:49-63 (1998).
 [4]
 RN FARNESYLATION
 RP MEDLINE=20459117; PubMed=10852915; DOI=10.1074/jbc.M003469200;
 RX Ashar H.R., James L., Gray K., Carr D., Black S., Armstrong L.;
 RA Bishop W.R., Kirschmeier P.;
 RT "Farnesyl transferase inhibitors block the farnesylation of CENP-E and
 RT CENP-F and alter the association of CENP-E with the microtubules.";
 RL J. Biol. Chem. 275:30451-30457 (2000).
 CC -!- FUNCTION: Minus-end directed microtubule motor. Probable
 CC kinetochore motor. Accumulates just before mitosis at the G2 phase
 CC of the cell cycle. Probably important for chromosome movement
 CC and/or spindle elongation.
 CC -!- SUBUNIT: Interacts with CENP-F and BUBR1 kinase.
 CC -!- SUBCELLULAR LOCATION: Associates with kinetochores during
 CC congression, relocates to the spindle midzone at anaphase, and is
 CC quantitatively discarded at the end of the cell division.
 CC -!- SIMILARITY: Belongs to the kinesin-like protein family.
 CC -!- SIMILARITY: Contains 1 kinesin-motor domain.
 CC
 CC This Swiss-Prot entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use as long as its content is in no way modified and this statement is not
 CC removed.
 DR EMBL; Z15005; CAA78727.1; -; mRNA.
 DR FIR; S28261; S28261.
 DR PDB; IPTC; X-ray; A/B=2-342.
 DR Ensembl; ENSG00000138778; Homo sapiens.
 DR HGNC; HGNC:1856; CENPE.
 DR MIM; 117143; -.
 DR GO; GO:0000776; C:kinetochore; TAS.
 DR GO; GO:0005634; C:nucleus; TAS.
 DR GO; GO:0003777; F:microtubule motor activity; TAS.
 DR GO; GO:0000067; P:DNA replication and chromosome cycle; TAS.
 DR GO; GO:0007079; P:mitotic chromosome movement towards spindle. . .; TAS.
 DR GO; GO:0000089; P:mitotic metaphase; TAS.
 DR GO; GO:0007080; P:mitotic metaphase plate congression; TAS.
 DR InterPro; IPR001752; kinesin_motor.
 DR Pfam; PF00225; Kinesin; 1.
 DR PRINTS; PRO0380; KINESINHEAVY.
 DR SMART; SM00129; KISG; 1.
 DR PROSITE; PS00411; KINESIN_MOTOR_DOMAIN1; 1.
 DR PROSITE; PS00667; KINESIN_MOTOR_DOMAIN2; 1.
 KW 3D-structure; ATP-binding; Cell cycle; Cell division; Centromere;
 KW Coiled coil; Lipoprotein; Microtubule; Mitosis; Motor protein;
 KW Nucleotide-binding; Prenylation.
 FT DOMAIN 1 335 Kinesin-motor.
 FT NP_BIND 86 93 ATP (By similarity).
 FT REGION 2472 2663 Globular (Potential).
 FT COILED 336 2471 Potential.
 FT LIPID 2660 2660 S-farnesyl cysteine.

Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
Muroidea; Muridae; Murinae; Mus.
[1]
NCBI_TaxID=10090;
[1]
NUCLEOTIDE SEQUENCE.
SPRAIN=ICR;
MEDLINE=97420736; PubMed=9275178; DOI=10.1073/pnas.94.18.9654;
RA Nakagawa T., Tanaka Y., Matsuoka E., Kondo S., Okada Y., Noda Y.,
RA Kanai Y., Hirokawa N.;
RT "Identification and classification of 16 new kinesin superfamily (KIF)
RT proteins in mouse genome.";
RL Proc. Natl. Acad. Sci. U.S.A. 94:9654-9659(1997).
DR ENBL; AB00426; BAA22386.1; -; mRNA.
DR HSSP; P17119; 1F9V.
DR SMR; O35059; 1-154.
DR Ensembl; ENSMUSG0000045328; Mus musculus.
DR MGI; MGI:1098230; Cenpe.
DR GO; GO:000776; C.kinetochore; IDA.
DR GO; GO:0008608; P.attachment of spindle microtubules to kinet. .; TAS.
DR InterPro; IPR001752; kinesin_motor.
DR Pfam; PF00225; Kinesin; 1.
DR PRINTS; PR00380; KINESINHEAVY.
DR SMART; SM00129; KJSC; 1.
DR PROSITE; PS50067; KINESIN_MOTOR_DOMAIN2; 1.
KW ATP-binding; Microtubule; Kinesin; Motor protein; Nucleotide-binding.
FT NON_TER 1
FT NON_TER 160
FT NON_TER 160
SQ SEQUENCE 160 AA; 18406 MW; 9E6E4F6E2642C241 CRC64;
Query Match 89.9%; Score 71; DB 2; Length 160;
Best Local Similarity 93.3%; Pred. NO. 4.6e-05;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 RHYGETKMNQRRSS 15
||||| |||||||
DB 108 RHYGITKMNQRRSS 122

RESULT 5
Q7TPX4_MOUSE
ID Q7TPX4_MOUSE PRELIMINARY; PRT; 549 AA.
AC Q7TPX4;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Cenpe protein (Fragment).
GN Name=Cenpe;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muroidea; Muridae; Murinae; Mus.
ON NCBI_TaxID=10090;
OX [1]
NUCLEOTIDE SEQUENCE.
RP STRAIN=C57BL/6J; TISSUE=Egg;
RC MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haie F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udwin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullenby S.J.,
RA Bosak S.A., McWan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywicki M.I., Skalska U., Smailus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;

RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]

RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Egg;
RA Strausberg R.;
RL Submitted (MAY-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL: BC052843; AAHS2843.1; -, mRNA.
DR HSSP: P17119; 1F9T.
DR SMR: Q7TPX4; 4-339.
DR Ensembl; ENSMUSG00000045328; Mus musculus.
DR MGI: MGI:1098230; Cenpe.
DR GO: GO:0000776; C:kinetochore; IDA.
DR GO: GO:0008608; P:attachment of spindle microtubules to kinet. . .; TAS.
DR InterPro; IPR001752; kinesin_motor.
DR Pfam; PF00225; Kinesin; 1.
DR PRINTS; PR00380; KINESINHEAVY.
DR SMART; SM00129; KISC; 1.
DR PROSITE; PS00411; KINESIN MOTOR DOMAIN1; 1.
DR PROSITE; PS50067; KINESIN MOTOR DOMAIN2; 1.
KW ATP-binding; Microtubule; Motor protein; Nucleotide-binding.
FT NON_TER 549 549
SQ SEQUENCE 549 AA; 62899 MW; B707C97DC9FB38D3 CRC64;

Query Match 89.9%; Score 71; DB 2; Length 549;
Best Local Similarity 93.3%; Pred. No. 0.0002;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 RHYGETKNQRRSRS 15
||||| ||||| |||||
DB 189 RHYGITKNQRRSRS 203

RESULT 6
Q6RT24 MOUSE
ID Q6RT24 MOUSE PRELIMINARY; PRT; 2474 AA.
AC Q6RT24;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Centromere associated protein-E.
GN Name=Cenpe;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]

RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=22806743; PubMed=12925705; DOI=10.1083/jcb.200303167;
RA Weaver B.A., Bonday Z.Q., Putkey F.R., Kops G.J., Silk A.D.,
RA Cleveland D.W.;
RA "Centromere-associated protein-E is essential for the mammalian
RT mitotic checkpoint to prevent aneuploidy due to single chromosome
RT loss.";
RL J. Cell Biol. 162:551-563(2003).
DR EMBL; AY493378; AAR85498.1; -, mRNA.
DR SMR; Q6RT24; 4-339.
DR Ensembl; ENSMUSG00000045328; Mus musculus.
DR MGI: MGI:1098230; Cenpe.
DR GO: GO:0000776; C:kinetochore; IDA.
DR GO: GO:0008608; P:attachment of spindle microtubules to kinet. . .; TAS.
DR InterPro; IPR001752; kinesin_motor.
DR Pfam; PF00225; Kinesin; 1.
DR PRINTS; PR00380; KINESINHEAVY.
DR SMART; SM00129; KISC; 1.
DR PROSITE; PS00411; KINESIN MOTOR DOMAIN1; 1.
DR PROSITE; PS50067; KINESIN MOTOR DOMAIN2; 1.
DR PROSITE; PS00213; LIPOCALIN; UNKNOWN 1.
KW ATP-binding; Microtubule; Motor protein; Nucleotide-binding.
SQ SEQUENCE 2474 AA; 286525 MW; BAF52DD6068A2903 CRC64;

Query Match 89.9%; Score 71; DB 2; Length 2474;
Best Local Similarity 93.3%; Pred. No. 0.0013;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 RHYGETKNQRRSRS 15
||||| ||||| |||||
DB 189 RHYGITKNQRRSRS 203

RESULT 7
O42263 XENLA
ID O42263 XENLA PRELIMINARY; PRT; 2954 AA.
AC O42263;
DT 01-JAN-1998 (TrEMBLrel. 05, Created)
DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Kinesin-related protein.
GN Name=XENP-E;
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;
OC Xenopodidae; Xenopus; Xenopus.
OX NCBI_TaxID=8355;
RN [1]

RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=98028574; PubMed=9363944; DOI=10.1016/S0092-8674(00)80419-5;
RA Wood K.W., Sakowicz R., Goldstein L.S., Cleveland D.W.;
RT "CENP-E is a plus end-directed kinetochore motor required for
RL metaphase chromosome alignment.";
RL Cell 91:357-366(1997).
DR EMBL; AF027728; AAC60300.1; -, mRNA.
DR PIR; T14156; T14156.
DR HSSP; P17119; 1F9T.
DR SMR; O42263; 6-339.
DR GO: GO:0005874; C:Microtubule; IEA.
DR GO: GO:0005875; C:Microtubule associated complex; IEA.
DR GO: GO:0005524; F:ATP binding; IEA.
DR GO: GO:0003777; F:Microtubule motor activity; IEA.
DR GO: GO:0007018; P:Microtubule-based movement; IEA.
DR InterPro; IPR001752; kinesin_motor.
DR Pfam; PF00225; Kinesin; 1.
DR PRINTS; PR00380; KINESINHEAVY.
DR SMART; SM00129; KISC; 1.
DR PROSITE; PS00411; KINESIN MOTOR DOMAIN1; 1.
DR PROSITE; PS50067; KINESIN MOTOR DOMAIN2; 1.
KW ATP-binding; Microtubule; Motor protein; Nucleotide-binding.
SQ SEQUENCE 2954 AA; 339968 MW; 439804ED0E592679 CRC64;

Query Match 87.3%; Score 69; DB 2; Length 2954;
Best Local Similarity 86.7%; Pred. No. 0.0037;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 RHYGETKNQRRSRS 15
||||| ||||| |||||
DB 187 RHYGETKNQRRSRS 201

RESULT 8
Q94HV9 ARATH
ID Q94HV9 ARATH PRELIMINARY; PRT; 807 AA.
AC Q94HV9;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Kinesin motor protein (Kin2), putative.
GN Name=KIN14.11;
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
OC rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsids.
OX NCBI_TaxID=3702;
RN [1]

RP NUCLEOTIDE SEQUENCE.
 RA Town C.D., Haas B.J., Wu D., Maiti R., Hannick L.I., Chan A.P., T.V.,
 RA Tallon L.J., Rooney T., Utterback T.R., VanAken S.E., Feldblyum T.V.,
 RA White O., Fraser C.M.;
 RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
 RN NUCLEOTIDE SEQUENCE.
 RP NUCLEOTIDE SEQUENCE.
 RA Lin X., Kaul S.;
 RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
 RN NUCLEOTIDE SEQUENCE.
 RA Town C.D., Kaul S.;
 RL Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.
 RL EMBL; AC027036; AAK62792.1; -, Genomic_DNA.
 DR HSP; P20480; IN6M.
 DR GO; GO:0005874; C:microtubule; IEA.
 DR GO; GO:0005875; C:microtubule associated complex; IEA.
 DR GO; GO:0005524; F:ATP binding; IEA.
 DR GO; GO:0003777; F:microtubule motor activity; IEA.
 DR GO; GO:0007018; F:microtubule-based movement; IEA.
 DR InterPro; IPR001752; kinesin_motor.
 DR Pfam; PF00225; Kinesin; 1.
 DR PRINTS; PR00380; KINESINHEAVY.
 DR SMART; SM00129; KISC; 1.
 DR PROSITE; PS00411; KINESIN_MOTOR_DOMAIN1; 1.
 DR PROSITE; PS0067; KINESIN_MOTOR_DOMAIN2; 1.
 KW ATP-binding; Microtubule; Motor protein; Nucleotide-binding.
 SQ SEQUENCE 807 AA; 91261 MW; FD7CDAD68EA30C28 CRC64;

Query Match 73.4%; Score 58; DB 2; Length 807;
 Best Local Similarity 73.3%; Pred. No. 0.095; Mismatches 1; Indels 3; Gaps 0;
 Matches 11; Conservative 1; Mismatches 1; Indels 3; Gaps 0;

QY 1 RHYGETKNQSRSS 15
 Db 184 RHFGTNNVHSSRS 198
 ||:|||||

RESULT 9
 Q9S7P3 ARATH
 ID Q9S7P3 ARATH PRELIMINARY; PRT; 823 AA.
 AC Q9S7P3
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-FEB-2005 (TrEMBLrel. 29, Last annotation update)
 DE Kinesin-like protein.
 GN Name=ZCP125;
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
 OC rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsi.
 OX NCBI_TaxID=3702;
 RN NUCLEOTIDE SEQUENCE.
 RP NUCLEOTIDE SEQUENCE.
 RA Cheuk R., Shinn P., Brooks S., Buehler E., Chao Q., Johnson-Hopson C.,
 RA Khan S., Kim C., Altafi H., Bei B., Chin C., Chiou J., Choi E.,
 RA Conn L., Conway A., Gonzalez A., Hansen N., Howing B., Koo T., Lam B.,
 RA Lee J., Lenz C., Li J., Liu A., Liu J., Liu S., Mukharsy N.,
 RA Nguyen M., Palm C., Pham P., Sakano H., Schwartz J., Southwick A.,
 RA Thaveri A., Toriumi M., Vaysberg M., Yu G., Davis R., Federspiel N.,
 RA Theologis A., Ecker J.;
 RL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AC009317; AAF79747.1; -, Genomic_DNA.
 DR PIR; D96619; D96619.
 DR HSP; P20480; IN6M.
 DR GO; GO:0005874; C:microtubule; IEA.
 DR GO; GO:0005875; C:microtubule associated complex; IEA.
 DR GO; GO:0005524; F:ATP binding; IEA.
 DR GO; GO:0003777; F:microtubule motor activity; IEA.
 DR GO; GO:0007018; F:microtubule-based movement; IEA.
 DR InterPro; IPR001752; kinesin_motor.
 DR Pfam; PF00225; Kinesin; 1.
 DR PRINTS; PR00380; KINESINHEAVY.
 DR SMART; SM00129; KISC; 1.
 DR PROSITE; PS00411; KINESIN_MOTOR_DOMAIN1; 1.
 DR PROSITE; PS0067; KINESIN_MOTOR_DOMAIN2; 1.
 KW ATP-binding; Microtubule; Motor protein; Nucleotide-binding.
 SQ SEQUENCE 888 AA; 100695 MW; 0D640FBACEE01B5 CRC64;

Query Match 73.4%; Score 58; DB 2; Length 888;
 Best Local Similarity 73.3%; Pred. No. 0.11; Mismatches 1; Indels 3; Gaps 0;
 Matches 11; Conservative 1; Mismatches 1; Indels 3; Gaps 0;

QY 1 RHYGETKNQSRSS 15
 Db 215 RHFGTNNVHSSRS 229
 ||:|||||

DR Pfam; PF00225; Kinesin; 1.
 DR PRINTS; PR00380; KINESINHEAVY.
 DR SMART; SM00129; KISC; 1.
 DR PROSITE; PS00411; KINESIN_MOTOR_DOMAIN1; 1.
 DR PROSITE; PS0067; KINESIN_MOTOR_DOMAIN2; 1.
 KW ATP-binding; Microtubule; Motor protein; Nucleotide-binding.
 SQ SEQUENCE 823 AA; 93149 MW; 6AFB1C622B4632C9 CRC64;

Query Match 73.4%; Score 58; DB 2; Length 823;
 Best Local Similarity 73.3%; Pred. No. 0.098; Mismatches 1; Indels 3; Gaps 0;
 Matches 11; Conservative 1; Mismatches 1; Indels 3; Gaps 0;

QY 1 RHYGETKNQSRSS 15
 Db 184 RHFGTNNVHSSRS 198
 ||:|||||

RESULT 10
 Q9LQ62 ARATH
 ID Q9LQ62 ARATH PRELIMINARY; PRT; 888 AA.
 AC Q9LQ62;
 DT 01-OCT-2000 (TrEMBLrel. 15, Created)
 DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE T30516.9.
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
 OC rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsi.
 OX NCBI_TaxID=3702;
 RN NUCLEOTIDE SEQUENCE.
 RP NUCLEOTIDE SEQUENCE.
 RA Chao Q., Brooks S., Buehler E., Dunn P., Khan S., Kim C., Shinn P.,
 RA Altafi H., Araujo R., Conn L., Conway A.B., Gonzalez A., Hansen N.F.,
 RA Huizar L., Kremenetskaia I., Lenz C., Li J., Liu S., Luros S.,
 RA Rowley D., Schwartz J., Toriumi M., Vysotskaia V., Yu G., Davis R.W.,
 RA Federspiel N.A., Theologis A., Ecker J.R.;
 RL Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AC009317; AAF79747.1; -, Genomic_DNA.
 DR PIR; D96619; D96619.
 DR HSP; P20480; IN6M.
 DR GO; GO:0005874; C:microtubule; IEA.
 DR GO; GO:0005875; C:microtubule associated complex; IEA.
 DR GO; GO:0005524; F:ATP binding; IEA.
 DR GO; GO:0003777; F:microtubule motor activity; IEA.
 DR GO; GO:0007018; F:microtubule-based movement; IEA.
 DR InterPro; IPR001752; kinesin_motor.
 DR Pfam; PF00225; Kinesin; 1.
 DR PRINTS; PR00380; KINESINHEAVY.
 DR SMART; SM00129; KISC; 1.
 DR PROSITE; PS00411; KINESIN_MOTOR_DOMAIN1; 1.
 DR PROSITE; PS0067; KINESIN_MOTOR_DOMAIN2; 1.
 KW ATP-binding; Microtubule; Motor protein; Nucleotide-binding.
 SQ SEQUENCE 888 AA; 100695 MW; 0D640FBACEE01B5 CRC64;

Query Match 73.4%; Score 58; DB 2; Length 888;
 Best Local Similarity 73.3%; Pred. No. 0.11; Mismatches 1; Indels 3; Gaps 0;
 Matches 11; Conservative 1; Mismatches 1; Indels 3; Gaps 0;

QY 1 RHYGETKNQSRSS 15
 Db 215 RHFGTNNVHSSRS 229
 ||:|||||

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RESULT 11
Q7Q5F1 ANOGA
ID Q7Q5F1 ANOGA PRELIMINARY; PRT; 842 AA.
AC Q7Q5F1;
DT 01-MAR-2004 (TrEMBLrel. 26, Created)
DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE ENSANGP0000013488 (Fragment).
GN ORFNames=ENSANGG0000010999;
OS Anopheles gambiae str. PEST.
OC Eukaryota; Metazoa; Arthropoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea, Culicidae;
OC Anophelinae; Anophelinae.
OC NCBI_TaxID=180454;
OX [1]
RN NUCLEOTIDE SEQUENCE.
RP RP NUCLEOTIDE SEQUENCE.
RC STRAIN=PEST;
RG The Anopheles gambiae Sequence Committee;
RT "Anopheles gambiae re-annotation,";
RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=PEST;
RG The Anopheles gambiae Sequence Committee;
RL Submitted (APR-2004) to the EMBL/GenBank/DBJ databases.
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
CC EMBL; AAAAB01008960; EAA11882.2; -; Genomic_DNA.
DR GO; GO:0005874; C:microtubule; IEA.
DR GO; GO:0005875; C:microtubule associated complex; IEA.
DR GO; GO:0005875; C:microtubule associated complex; IEA.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0003777; F:microtubule motor activity; IEA.
DR GO; GO:0007018; P:microtubule-based movement; IEA.
DR InterPro; IPR001752; Kinesin motor.
DR InterPro; IPR002017; Spectrin.
DR Pfam; PF00225; Kinesin; 1.
DR PRINTS; PR00380; KINESINHEAVY.
DR SMART; SM00129; KISC; 1.
DR PROSITE; PS0067; KINESIN MOTOR DOMAIN2; 1.
KW ATP-binding; Microtubule; Motor protein; Nucleotide-binding.
FT NON TER 1 842
FT NON TER 842 842
SQ SEQUENCE 842 AA; 95303 MW; 745DB46FALCDBCCC CRC64;

Query Match 68.4%; Score 54; DB 2; Length 842;
Best Local Similarity 73.3%; Pred. No. 0.58;
Matches 11; Conservative 1; Mismatches 3; Indels 0; Gaps 0

Qy 1 RHYGETKNQRRSRS 15
| ||| |||||
Db 125 RKIGETNNRRSRS 139

RESULT 12
Q6IWZ2 LEIDO
ID Q6IWZ2 LEIDO PRELIMINARY; PRT; 859 AA.
AC Q6IWZ2;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Kinesin related protein (Fragment).
OS Leishmania donovani.
OC Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae; Leishmania.
OC NCBI_TaxID=5661;
OX [1]
RN NUCLEOTIDE SEQUENCE.
RP RP NUCLEOTIDE SEQUENCE.
RC STRAIN=KEL6;
RA Sivakumar R., Singh S.;
RL Submitted (MAY-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY615886; AAT40474.1; -; Genomic_DNA.
DR GO; GO:0005874; C:microtubule; IEA.

```


GN Names=KIN;
 OS Leishmania chagasi.
 OC Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae; Leishmania.
 OX NCBI_TaxID=44211;
 [1]
 RN NUCLEOTIDE SEQUENCE.
 RC STRAIN=NHOM/BR/82/BA-2;
 RX MEDLINE=93133867; PubMed=8421715;
 RA Burns J.M. Jr., Shreffler W.G., Benson D.R., Ghalib H.W., Badaro R.,
 RT "Molecular characterization of a kinesiin-related antigen of Leishmania
 RT chagasi that detects specific antibody in African and American
 RT visceral leishmaniasis";
 RL Proc. Natl. Acad. Sci. U.S.A. 90:775-779(1993).
 CC -1- DEVELOPMENTAL STAGE: Predominant in amastigotes.
 CC -1- SIMILARITY: Belongs to the kinesiin-like protein family.
 CC -1- SIMILARITY: Contains 1 kinesiin-motor domain.
 CC -----
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 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use as long as its content is in no way modified and this statement is not
 CC removed.
 CC -----
 DR EMBL; L07879; AAA29254.1; -; Genomic_DNA.
 DR PIR; A47334; A47334.
 DR HSP; P17119; 3KAR.
 DR InterPro; IPR001752; kinesiin_motor.
 DR Pfam; PF00225; Kinesin; 1.
 DR PRINTS; PR00380; KINESINHEAVY.
 DR SMART; SM00129; KISC; 1.
 DR PROSITE; PS00411; KINESIN MOTOR DOMAIN1; 1.
 DR PROSITE; PS00667; KINESIN MOTOR DOMAIN2; 1.
 KW ATP-binding; Coiled coil; Microtubule; Motor protein;
 KW Nucleotide-binding; Repeat.
 FT DOMAIN 1 399 Kinesiin-motor.
 FT REPEAT 704 742 1.
 FT REPEAT 743 781 2.
 FT REPEAT 782 820 3.
 FT REPEAT 821 859 4.
 FT REPEAT 860 898 5.
 FT REPEAT 899 937 6.
 FT REPEAT 938 955 7 (partial).
 FT NP_BIND 122 129 ATP (potential).
 FT REGION 704 >955 7 X 39 AA approximate tandem repeats.
 FT COILED 426 >955 Potential.
 FT NON_TER 955 955
 SQ SEQUENCE 955 AA; 106168 MW; 8CA76815BE84C6E9 CRC64;
 Query Match 68.4%; Score 54; DB 1; Length 955;
 Best Local Similarity 73.3%; Pred. No. 0.67;
 Matches 11; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
 QY 1 RHYGETKNQSSRS 15
 DB 241 RQKGETKNQSSRS 255
 RESULT 15
 Q57UD0_9TRYP PRELIMINARY; PRT; 1803 AA.
 AC Q57UD0;
 DT 10-MAY-2005 (TrEMBLrel. 30, Created)
 DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
 DT 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
 DE Kinesin K39, putative.
 GN ORFNames=TB927.7.3830;
 OS Trypanosoma brucei.
 OC Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae; Trypanosoma.
 OX NCBI_TaxID=5691;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=GUTat10.1;

RA Ghedin E., Blandin G., Bartholomeu D., Caler E., Haas B., Hannick L.,
 RA Shallom J., Hou L., Djikeng A., Feldblyum T., Hostetler J.,
 RA Johnson J., Jones K., Koo H.L., Larkin C., Pai G., Peterson J.,
 RA Khalak H.G., Salzberg S., Simpson A.J., Tallon L., Van Aken S.,
 RA Wanless D., White O., Wortman J., Fraser C.M., El-Sayed N.M.A.;
 RL Submitted (APR-2005) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AC159454; AAX70789.1; -; Genomic DNA.
 SQ SEQUENCE 1803 AA; 206481 MW; 440EAD009C0E67A CRC64;
 Query Match 68.4%; Score 54; DB 2; Length 1803;
 Best Local Similarity 73.3%; Pred. No. 1.5;
 Matches 11; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
 QY 1 RHYGETKNQSSRS 15
 DB 256 RHTASTKNQSSRS 270
 RESULT 16
 Q57V46_9TRYP PRELIMINARY; PRT; 578 AA.
 ID Q57V46;
 AC Q57V46;
 DT 10-MAY-2005 (TrEMBLrel. 30, Created)
 DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
 DT 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
 DE Kinesin, putative.
 GN ORFNames=TB927.3.3400;
 OS Trypanosoma brucei.
 OC Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae; Trypanosoma.
 OX NCBI_TaxID=5691;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=GUTat10.1;
 RA Ghedin E., Blandin G., Bartholomeu D., Caler E., Haas B., Hannick L.,
 RA Shallom J., Hou L., Djikeng A., Feldblyum T., Hostetler J.,
 RA Johnson J., Jones K., Koo H.L., Larkin C., Pai G., Peterson J.,
 RA Khalak H.G., Salzberg S., Simpson A.J., Tallon L., Van Aken S.,
 RA Wanless D., White O., Wortman J., Fraser C.M., El-Sayed N.M.A.;
 RL Submitted (APR-2005) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AC159446; AAX70522.1; -; Genomic_DNA.
 DR GO; GO:0005874; C:Microtubule; IEA.
 DR GO; GO:0005875; C:Microtubule associated complex; IEA.
 DR GO; GO:0005524; P:ATP binding; IEA.
 DR GO; GO:0003777; F:Microtubule motor activity; IEA.
 DR GO; GO:0007018; P:Microtubule-based movement; IEA.
 DR InterPro; IPR002198; ADH short.
 DR InterPro; IPR001752; Kinesin_motor.
 DR Pfam; PF00225; Kinesin; 1.
 DR PRINTS; PR00380; KINESINHEAVY.
 DR SMART; SM00129; KISC; 1.
 DR PROSITE; PS00061; ADH_SHORT; UNKNOWN 1.
 DR PROSITE; PS00067; KINESIN MOTOR DOMAIN2; 1.
 SQ SEQUENCE 578 AA; 63787 MW; 1A0AD46C254E49D CRC64;
 Query Match 67.1%; Score 53; DB 2; Length 578;
 Best Local Similarity 73.3%; Pred. No. 0.57;
 Matches 11; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
 QY 1 RHYGETKNQSSRS 15
 DB 201 RQKGETKNQSSRS 215
 RESULT 17
 Q57V47_9TRYP PRELIMINARY; PRT; 591 AA.
 ID Q57V47;
 AC Q57V47;
 DT 10-MAY-2005 (TrEMBLrel. 30, Created)
 DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
 DT 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
 DE Kinesin, putative.
 GN ORFNames=TB927.3.3390;
 OS Trypanosoma brucei.

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OC Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae; Trypanosoma.
OX NCBI_TaxID=5691;
RN [1]
RC STRAIN-GUTRat10.1;
RA Ghedin E., Blandin G., Bartholomeu D., Caler E., Haas B., Hannick L.,
RA Shallow J., Hou L., Djikeng A., Feldblum T., Hostetler J.,
RA Johnson J., Jones K., Koo H.L., Larkin C., Pai G., Peterson J.,
RA Khalak H.G., Salzberg S., Simpson A.J., Tallon L., Van Aken S.,
RA Wanless D., White O., Wortman J., Fraser C.M., El-Sayed N.M.A.;
RL Submitted (APR-2005) to the EMBL/GenBank/DBJ databases.
DR EMBL; AC159446; AAX70521.1; -; Genomic DNA.
SQ SEQUENCE 591 AA; 65845 MW; 82B4E0AE6582B4EB CRC64;

Query Match 67.1%; Score 53; DB 2; Length 591;
Best Local Similarity 73.3%; Pred. No. 0.58;
Matches 11; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 RHYGETKNQRSRS 15
Db 201 RQKGETKNQTSRS 215

RESULT 18
Q4QFW3 LEIMA
ID Q4QFW3 LEIMA PRELIMINARY; PRT; 1229 AA.
AC Q4QFW3
DT 13-SEP-2005 (TreeBLrel. 31, Created)
DT 13-SEP-2005 (TreeBLrel. 31, Last sequence update)
DE Kinesin K39, putative.
GN ORFNames=lmjF14.1110;
OS Leishmania major.
OC Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae; Leishmania.
OX NCBI_TaxID=5664;
RN [1]
RC STRAIN=Friedlin;
RA Peacock C.S., Murphy L., Ivens A.C., Beriman M., Blackwell J.,
RA Smith D., Collins M., Fosker N., Harris D., Oliver K., O'Neil S.,
RA Saunders D., Seeger K., Warren T., Apostolou Z., Bauser C., Beck A.,
RA Bianchetti G., Borzym K., Bothé G., Bruschi C., Clarioni L.,
RA Duesterhoeft A., Fuchs M., Gabel C., Goffeau A., Hilbert H.,
RA Klages S., Kube M., Marra M., Masuy D., Mueller-Auer S., Pohl T.,
RA Purnelle B., Reinhardt R., Rieger M., Robben J., Schaefer M.,
RA Tosato V., Volckaert G., Wambut R., Wedler H., Zimmermann M.,
RA Rajandream M., and Barrall B.G.;
RL Submitted (JUN-2005) to the EMBL/GenBank/DBJ databases.
DR EMBL; CT005253; CAJ03171.1; -; Genomic DNA.
SQ SEQUENCE 1229 AA; 137506 MW; 91EA1D70A2BAF92F CRC64;

Query Match 67.1%; Score 53; DB 2; Length 1229;
Best Local Similarity 73.3%; Pred. No. 1.4;
Matches 11; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 RHYGETKNQRSRS 15
Db 211 RHTAATKNQRSRS 225

RESULT 19
Q5VK10 DROME
ID Q5VK10 DROME PRELIMINARY; PRT; 2013 AA.
AC Q5VK10
DT 01-MAY-2000 (TreeBLrel. 13, Created)
DT 01-MAY-2000 (TreeBLrel. 16, Last sequence update)
DT 01-MAY-2004 (TreeBLrel. 26, Last annotation update)
DE CG6392-PA.
GN Name=cnet; ORFNames=CG6392;
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.

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OX NCBI_TaxID=7227;
RN [1]
RC NUCLEOTIDE SEQUENCE.
RX MEDLINE=20196006; PubMed=10731132; DOI=10.1126/science.287.5461.2185;
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brotter P.,
RA Burtis K.C., Buesam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Kocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
RA Foeller C., Gabriellian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D.A., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwan C.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Laoko P., Lei Y., Levitsky A.A., Li J.H., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milghina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nuskern D.R., Pacle J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Klamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier B., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zhong X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
"Finishing a whole-genome shotgun: release 3 of the Drosophila
melanogaster euchromatic genome sequence."
The genome sequence of Drosophila melanogaster.;
Science 287:2185-2195(2000).
[2]
RC NUCLEOTIDE SEQUENCE.
RX MEDLINE=22426065; PubMed=12537568;
RA Celniker S.E., Wheeler D.A., Kronmiller B., Carlson J.W., Halpern A.,
RA Patel S., Adams M., Champe M., Dugan S.P., Frise E., Hodgson A.,
RA George R.A., Hoskins R.A., Laverly T., Muzny D.M., Nelson C.R.,
RA Pacle J.M., Park S., Pfeiffer B.D., Richards S., Sodergren E.J.,
RA Svirskas R., Tabor P.E., Wan K., Stapleton M., Sutton G.G., Venter C.,
RA Weinstock G., Scherer S.E., Myers E.W., Gibbs R.A., Rubin G.M.;
"Finishing a whole-genome shotgun: release 3 of the Drosophila
melanogaster euchromatic genome sequence."
Genome Biol. 3:RESEARCH0079-RESEARCH0079(2002).
[3]
RC NUCLEOTIDE SEQUENCE.
RX MEDLINE=22426070; PubMed=12537573;
RA Kaminker J.S., Bergman C.M., Kronmiller B., Carlson J.W., Svirskas R.,
RA Patel S., Frise E., Wheeler D.A., Lewis S.E., Rubin G.M.,
RA Ashburner M., Celniker S.E.;
"The transposable elements of the Drosophila melanogaster euchromatin:
a genomics perspective."
Genome Biol. 3:RESEARCH0084.1-RESEARCH0084.20(2002).
[4]
RC NUCLEOTIDE SEQUENCE
RX MEDLINE=22426065; PubMed=12537572;
RA Mira S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,
RA Hradecky P., Huang Y., Kaminker J.S., Millburn G.H., Prochuk S.E.,
RA Smith C.D., Tupy J.L., Whitfield E.J., Bayraktaroglu L., Berman B.P.,
RA Bettencourt B.R., Celniker S.E., de Grey A.D.N.J., Drysdale R.A.,
RA Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q.,
RA Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
Lewis S.E.;

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RT "Annotation of the Drosophila melanogaster euchromatic genome: a systematic review.";
 RL Genome Biol. 3:RESEARCH0083.1-RESEARCH0083.22(2002).
 RN [5]
 RP NUCLEOTIDE SEQUENCE.
 RG Berkeley Drosophila Genome Project;
 RA Celisner S., Carlson J., Wan K., Pfeiffer B., Frise E., George R.,
 RA Hoskins R., Scapleton M., Facieb J., Park S., Svirskas R., Smith E.,
 RA Yu C., Rubin G.;
 RT "Drosophila melanogaster release 4 sequence.";
 RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
 RN [6]
 RP NUCLEOTIDE SEQUENCE.
 RG FlyBase;
 RL Submitted (MAR-2005) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AE003631; AAF53088.2; -; Genomic DNA.
 DR HSP; P17119; 1F9T.
 DR FlyBase; FBgn0040232; cmet.
 DR GO; GO:0000776; C:kinetochore; IDA.
 DR GO; GO:0000940; C:outer kinetochore of condensed chromosome; NAS.
 DR GO; GO:0007049; P:cell cycle; IMP.
 DR GO; GO:0007080; P:mitotic metaphase plate congression; IMP.
 DR InterPro; IPR000074; ApoA1_A4_E.
 DR InterPro; IPR001752; kinesin motor.
 DR PRINTS; PF00225; Kinesin; 1.
 DR SMART; SM00129; KISC; 1.
 DR SMART; SM00150; SPEC; 3.
 DR PROSITE; PS00411; KINESIN MOTOR DOMAIN1; 1.
 DR PROSITE; PS50067; KINESIN MOTOR DOMAIN2; 1.
 DR ATP-binding; Microtubule; Motor protein; Nucleotide-binding.
 KW SEQUENCE 2013 AA; 231110 MW; 8A1A46581EF4F5F CRC64;
 SQ

Query Match 67.1%; Score 53; DB 2; Length 2013;
 Best Local Similarity 73.3%; Pred. No. 2.6; Mismatches 3; Indels 0; Gaps 0;
 Matches 11; Conservative 1;

QY 1 RHYGETKNQRRSS 15
 |||||
 DB 183 RTVGETNNRRSS 197

RESULT 20
 QNCGO DROME PRELIMINARY; PRT; 2244 AA.
 AC QNCGO;
 DT 01-OCT-2000 (TrEMBLrel. 15, Created)
 DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE Kinesin-like kinetochore motor protein CENP-meta.
 GN Name=cmet; ORFNames=CG6392;
 OS Drosophila melanogaster (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydroidea; Drosophilidae; Drosophila.
 OX NCBI_TaxID=7227;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RX MEDLINE=20351410; PubMed=10893249; DOI=10.1083/jcb.150.1.1;
 RA Yudel J.K., Marsalek J.D., McIntosh J.R., Goldstein L.S.B.,
 RA Cleveland D.W., Philip A.V.;
 RT "CENP-meta, an essential kinetochore protein required for the maintenance of metaphase chromosome alignment in Drosophila.";
 RL J. Cell Biol. 150:1-11(2000).
 DR EMBL; AF220353; AAF32355.1; -; mRNA.
 DR HSP; P17119; 1F9T.
 DR FlyBase; FBgn0040232; cmet.
 DR GO; GO:0000776; C:kinetochore; IDA.
 DR GO; GO:0000940; C:outer kinetochore of condensed chromosome; NAS.
 DR GO; GO:0007049; P:cell cycle; IMP.
 DR GO; GO:0007080; P:mitotic metaphase plate congression; IMP.
 DR InterPro; IPR000074; ApoA1_A4_E.

DR InterPro; IPR001752; kinesin_motor.
 DR Pfam; PF00225; Kinesin; 1.
 DR PRINTS; PR00380; KINESINHEAVY.
 DR SMART; SM00129; KISC; 1.
 DR PROSITE; PS00411; KINESIN MOTOR DOMAIN1; 1.
 DR PROSITE; PS50067; KINESIN MOTOR DOMAIN2; 1.
 KW ATP-binding; Microtubule; Motor protein; Nucleotide-binding.
 SQ SEQUENCE 2244 AA; 257994 MW; FA6AA3B2A541ADE0 CRC64;

Query Match 67.1%; Score 53; DB 2; Length 2244;
 Best Local Similarity 73.3%; Pred. No. 2.9; Mismatches 3; Indels 0; Gaps 0;
 Matches 11; Conservative 1;

QY 1 RHYGETKNQRRSS 15
 |||||
 DB 183 RTVGETNNRRSS 197

RESULT 21
 Q4QFM4_LEIMA PRELIMINARY; PRT; 2765 AA.
 AC Q4QFM4;
 DT 13-SEP-2005 (TrEMBLrel. 31, Created)
 DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
 DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
 DE Kinesin K39, putative.
 GN ORFNames=LmjF14.1100;
 OS Leishmania major.
 OC Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae; Leishmania.
 OX NCBI_TaxID=5664;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=Friedlin;
 RA Peacock C.S., Murphy L., Ivens A.C., Berriman M., Blackwell J.,
 RA Smith D., Collins M., Foster N., Harris D., Oliver K., O'Neill S.,
 RA Saunders D., Seeger K., Warren T., Apostolou Z., Bauser C., Beck A.,
 RA Bianchetti G., Borzym K., Bothe G., Bruschi C., Clarioni L.,
 RA Dusterhoef A., Fuchs M., Gabel C., Goffeau A., Hilbert H.,
 RA Klages S., Kube M., Marra M., Masuy D., Mueller-Auer S., Pohl T.,
 RA Purnelle B., Reinhardt R., Rieger M., Robben J., Schaefer M.,
 RA Tosato V., Volckaert G., Wambutt R., Wedler H., Zimmermann M.,
 RA Rajandream M., and Barrell B.G.;
 RL Submitted (JUN-2005) to the EMBL/GenBank/DBJ databases.
 DR EMBL; CT005253; CAJ03170.1; -; Genomic DNA.
 SQ SEQUENCE 2765 AA; 301723 MW; C78191359345FA CRC64;

Query Match 67.1%; Score 53; DB 2; Length 2765;
 Best Local Similarity 73.3%; Pred. No. 3.8; Mismatches 4; Indels 0; Gaps 0;
 Matches 11; Conservative 0;

QY 1 RHYGETKNQRRSS 15
 |||||
 DB 241 RHTAATKNDRSS 255

RESULT 22
 Q4QFM2_LEIMA PRELIMINARY; PRT; 2976 AA.
 AC Q4QFM2;
 DT 13-SEP-2005 (TrEMBLrel. 31, Created)
 DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
 DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
 DE Kinesin K39, putative.
 GN ORFNames=LmjF14.1120;
 OS Leishmania major.
 OC Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae; Leishmania.
 OX NCBI_TaxID=5664;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=Friedlin;
 RA Peacock C.S., Murphy L., Ivens A.C., Berriman M., Blackwell J.,
 RA Smith D., Collins M., Foster N., Harris D., Oliver K., O'Neill S.,
 RA Saunders D., Seeger K., Warren T., Apostolou Z., Bauser C., Beck A.,

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RA Bianchetti G., Borzym K., Bothe G., Bruschi C., Ciarloni L.,
RA Duesterhoeft A., Fuchs M., Gabel C., Goffeau A., Hilbert H.,
RA Klages S., Kube M., Marra M., Masuy D., Mueller-Auer S., Pohl T.,
RA Purnelle B., Reinhardt R., Rieger M., Robben J., Schaefer M.,
RA Toato V., Volckaert G., Wambütt R., Wedler H., Zimmermann M.,
RA Rajandream M., and Barrall B.G.;
RL Submitted (JUN-2005) to the EMBL/GenBank/DBJ databases.
DR EMBL; CTO05253; CAJ03172.1; -; Genomic DNA.
SQ SEQUENCE 2976 AA; 341140 MW; 0283F8FB4848050D CRC64;

Query Match 67.1%; Score 53; DB 2; Length 2976;
Best Local Similarity 73.3%; Pred. No. 4.1;
Matches 11; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 RHYGETKNQRSSRS 15
||| ||| ||| ||| |||
Db 185 RHTAATKNDRSSRS 199

RESULT 23
O54722 RAT PRELIMINARY; PRT; 168 AA.
AC O54722;
DT 01-JUN-1998 (TrEMBLrel. 06, Created)
DT 01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
DE 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Kinesin-related protein KRP5 (Fragment).
GN Name=Krp5; Synonyms=KRPS;
OS Rattus norvegicus (Rat)...
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=Sprague-Dawley; TISSUE=Testes;
RX MEDLINE=96228687; PubMed=8688559;
RA Sperry A.O.; Zhao L.-P.;
RT "Kinesin-related proteins in the mammalian testes: candidate motors
RT for meiosis and morphogenesis";
RL Mol. Biol. Cell 7:289-305(1996).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=Sprague-Dawley; TISSUE=Testes;
RA Sperry A.O.;
RL Submitted (NOV-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF035954; AAB88702.1; -; mRNA.
DR HSSP; P17119; IF9V.
DR Ensembl; ENSRNOG0000019257; Rattus norvegicus.
DR RGD; 621071; Krp5.
DR GO; GO:0005874; C:microtubule; IEA.
DR GO; GO:0005875; C:microtubule associated complex; IEA.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0003777; F:microtubule motor activity; IEA.
DR GO; GO:0007018; P:microtubule-based movement; IEA.
DR InterPro; IPR001752; kinesin_motor.
DR Pfam; PF00225; Kinesin; 1.
DR SMART; SM00129; KISC; 1.
DR PROSITE; PS0067; KINESIN MOTOR DOMAIN2; 1.
KW ATP-binding; Microtubule; Motor protein; Nucleotide-binding.
FT NON TER 1
FT NON TER 168
SQ SEQUENCE 168 AA; 18752 MW; D961E4CDBDAAB7 CRC64;

Query Match 65.8%; Score 52; DB 2; Length 168;
Best Local Similarity 66.7%; Pred. No. 0.2;
Matches 10; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 1 RHYGETKNQRSSRS 15
||| ||| ||| ||| |||
Db 114 RHTGTTQNHSSRS 128

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RESULT 24
Q9SS30 ARATH PRELIMINARY; PRT; 459 AA.
AC Q9SS30;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DE 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Putative kinesin-like centromere protein.
GN Name=F14P13.22;
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
OC rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsids.
OX NCBI_TaxID=3702;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Lin X., Kaul S., Town C.D., Benito M.-I., Creasy T.H., Haas B.,
RA Ronning C.M., Koo H., Fujii C.Y., Utterback T.R., Barnstead M.E.,
RA Bowman C.L., White O., Nierman W.C., Fraser C.M.;
RL Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AC009400; AAF02823.1; -; Genomic DNA.
DR HSSP; P17119; IF9T.
DR GO; GO:0005874; C:microtubule; IEA.
DR GO; GO:0005875; C:microtubule associated complex; IEA.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0003777; F:microtubule motor activity; IEA.
DR GO; GO:0007018; P:microtubule-based movement; IEA.
DR InterPro; IPR001752; kinesin_motor.
DR Pfam; PF00225; Kinesin; 1.
DR PRINTS; PRO0380; KINESINHEAVY.
DR SMART; SM00129; KISC; 1.
DR PROSITE; PS00411; KINESIN MOTOR DOMAIN1; 1.
DR PROSITE; PS0067; KINESIN MOTOR DOMAIN2; 1.
KW ATP-binding; Microtubule; Motor protein; Nucleotide-binding.
SQ SEQUENCE 459 AA; 51972 MW; 7C8487E9B7038E6A CRC64;

Query Match 65.8%; Score 52; DB 2; Length 459;
Best Local Similarity 73.3%; Pred. No. 0.67;
Matches 11; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 RHYGETKNQRSSRS 15
||| ||| ||| ||| |||
Db 182 RHIGETNNLYSSRS 196

RESULT 25
Q57XT2 9TRYP PRELIMINARY; PRT; 810 AA.
AC Q57XT2;
DT 10-MAY-2005 (TrEMBLrel. 30, Created)
DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
DE 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
DE Kinesin, putative.
GN ORFNames=fb927.7-7120;
OS Trypanosoma brucei.
OC Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae; Trypanosoma.
OX NCBI_TaxID=5691;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=GUTat10.1;
RA Ghedin E., Blandin G., Bartholomeu D., Caler E., Haas B., Hannick L.,
RA Shallow J., Hou L., Djikeng A., Feldblyum T., Hostetler J.,
RA Johnson J., Jones K., Koo H.L., Larkin C., Pai G., Peterson J.,
RA Khalak H.G., Salzberg S., Simpson A.J., Tallon L., Van Aken S.,
RA Waless D., White O., Wortman J., Fraser C.M., El-Sayed N.M.A.;
RL Submitted (APR-2005) to the EMBL/GenBank/DBJ databases.
DR EMBL; AC159412; AAX69587.1; -; Genomic DNA.
DR GO; GO:0005874; C:microtubule; IEA.
DR GO; GO:0005875; C:microtubule associated complex; IEA.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0003777; F:microtubule motor activity; IEA.
DR GO; GO:0007018; P:microtubule-based movement; IEA.
DR InterPro; IPR001752; kinesin_motor.

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DR Pfam; PF00225; Kinesin; 1.
 DR PRINTS; PR00380; KINESINHEAVY.
 DR SMART; SM00129; KISC; 1.
 DR PROSITE; PS50067; KINESIN_MOTOR_DOMAIN2; 1.
 SQ SEQUENCE 810 AA; 87881 MW; B04AF497EAD787B4 CRC64;

Query Match 65.8%; Score 52; DB 2; Length 810;
 Best Local Similarity 66.7%; Pred. No. 1.3;
 Matches 10; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 RHYGETKNQSRSS 15
 DB 449 RHVGSTAVNQSRSS 463
 ||| | | | | | | | | |

RESULT 26
 Q95LL1 MACFA
 ID Q95LL1 MACFA PRELIMINARY; PRT; 865 AA.
 AC Q95LL1;
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE Hypothetical protein (Crab eating macaque)
 OS Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Euthera; Euarchontoglires; Primates; Catarrhini;
 OC Cercopitheidae; Cercopithecinæ; Macaca.
 OX NCBI_TaxID=9541;
 RN [1]
 RC NUCLEOTIDE SEQUENCE.
 RP TISSUE=Testis;
 RA Osada N., Hida M., Kusuda J., Tanuma R., Hirata M., Suto Y., Hirai M.,
 RA Terao K., Sugano S., Hashimoto K.;
 RT "Cynomolgus monkey testicular cDNAs for discovery of novel human genes
 in the human genome sequence."
 RL BMC Genomics 3:36-36(2002).
 DR EMBL; AB072777; BAB69746.1; -; mRNA.
 DR HSSP; P33173; 115S.
 DR GO; GO:0005874; C:Microtubule; IEA.
 DR GO; GO:0005875; C:Microtubule associated complex; IEA.
 DR GO; GO:0005524; F:ATP binding; IEA.
 DR GO; GO:0003777; F:Microtubule motor activity; IEA.
 DR GO; GO:0007018; P:Microtubule-based movement; IEA.
 DR InterPro; IPR001752; kinesin_motor.
 DR Pfam; PF00225; Kinesin; 1.
 DR PRINTS; PR00380; KINESINHEAVY.
 DR SMART; SM00129; KISC; 1.
 DR PROSITE; PS00411; KINESIN_MOTOR_DOMAIN1; UNKNOWN_1.
 DR PROSITE; PS50067; KINESIN_MOTOR_DOMAIN2; 1.
 KW ATP-binding; Hypothetical protein; Microtubule; Motor protein;
 KW Nucleotide-binding.
 FT NON_TER 865 865
 SQ SEQUENCE 865 AA; 98464 MW; 13341B786F448324 CRC64;

Query Match 65.8%; Score 52; DB 2; Length 865;
 Best Local Similarity 66.7%; Pred. No. 1.4;
 Matches 10; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 RHYGETKNQSRSS 15
 DB 193 RHTGTQWNEHSSRS 207
 ||| | | | | | | | | |

RESULT 27
 Q7PCK6 MACFA
 ID Q7PCK6 MACFA PRELIMINARY; PRT; 1266 AA.
 AC Q7PCK6;
 DT 01-MAR-2004 (TrEMBLrel. 26, Created)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE Kinesin-related protein KIF27.
 OS Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Euthera; Euarchontoglires; Primates; Catarrhini;
 OC Cercopitheidae; Cercopithecinæ; Macaca.
 OX NCBI_TaxID=9541;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RX MEDLINE=22730772; PubMed=12783626; DOI=10.1186/1471-2164-4-22;
 RA Oduru S., Campbell J.L., Karri S., Hendry W.J., Khan S.A.,
 RA Williams S.C.;
 RT "Gene discovery in the hamster: a comparative genomics approach for
 gene annotation by sequencing of hamster testis cDNAs."
 RL BMC Genomics 4:22-22(2003).
 CC -1- MISCELLANEOUS: The sequence shown here is derived from an
 CC EMBL/GenBank/DDJB third party annotation (TPA) entry.
 DR EMBL; BK001055; DAA01313.1; -; mRNA.
 DR HSSP; P33173; 115S.
 DR GO; GO:0005874; C:Microtubule; IEA.
 DR GO; GO:0005875; C:Microtubule associated complex; IEA.
 DR GO; GO:0005524; F:ATP binding; IEA.
 DR GO; GO:0003777; F:Microtubule motor activity; IEA.
 DR GO; GO:0007018; P:Microtubule-based movement; IEA.
 DR InterPro; IPR001752; kinesin_motor.
 DR Pfam; PF00225; Kinesin; 1.
 DR PRINTS; PR00380; KINESINHEAVY.
 DR PROSITE; PS00411; KINESIN_MOTOR_DOMAIN1; UNKNOWN_1.
 DR PROSITE; PS50067; KINESIN_MOTOR_DOMAIN2; 1.
 KW ATP-binding; Microtubule; Motor protein; Nucleotide-binding.
 SQ SEQUENCE 1266 AA; 144457 MW; DES8A8EB5CC6E CRC64;

Query Match 65.8%; Score 52; DB 2; Length 1266;
 Best Local Similarity 66.7%; Pred. No. 2.3;
 Matches 10; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 RHYGETKNQSRSS 15
 DB 193 RHTGTQWNEHSSRS 207
 ||| | | | | | | | | |

RESULT 28
 Q86VH0 HUMAN
 ID Q86VH0 HUMAN PRELIMINARY; PRT; 1304 AA.
 AC Q86VH0;
 DT 01-JUN-2003 (TrEMBLrel. 24, Created)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE KIF27C.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Euthera; Euarchontoglires; Primates; Catarrhini; Hominidae;
 OC Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RX MEDLINE=22730772; PubMed=12783626; DOI=10.1186/1471-2164-4-22;
 RA Oduru S., Campbell J.L., Karri S., Hendry W.J., Khan S.A.,
 RA Williams S.C.;
 RT "Gene discovery in the hamster: a comparative genomics approach for
 gene annotation by sequencing of hamster testis cDNAs."
 RL BMC Genomics 4:22-22(2003).
 DR EMBL; AY237538; AAP04415.1; -; mRNA.
 DR HSSP; P33173; 115S.
 DR Ensembl; ENSG00000165115; Homo sapiens.
 DR GO; GO:0005874; C:Microtubule; IEA.
 DR GO; GO:0005875; C:Microtubule associated complex; IEA.
 DR GO; GO:0005524; F:ATP binding; IEA.
 DR GO; GO:0003777; F:Microtubule motor activity; IEA.
 DR GO; GO:0007018; P:Microtubule-based movement; IEA.
 DR InterPro; IPR001752; kinesin_motor.
 DR Pfam; PF00225; Kinesin; 1.
 DR PRINTS; PR00380; KINESINHEAVY.
 DR SMART; SM00129; KISC; 1.
 DR PROSITE; PS00411; KINESIN_MOTOR_DOMAIN1; UNKNOWN_1.
 DR PROSITE; PS50067; KINESIN_MOTOR_DOMAIN2; 1.
 KW ATP-binding; Microtubule; Motor protein; Nucleotide-binding.

```
SQ SEQUENCE 1304 AA; 148978 MW; 7FEBD1BBC879016C CRC64;
Query Match 65.8%; Score 52; DB 2; Length 1304;
Best Local Similarity 66.7%; Pred. No. 2.4;
Matches 10; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 RHYGETKNQRSRS 15
Db 193 RHTGTTQNHSSRS 207

RESULT 29
Q86VH1 HUMAN
ID Q86VH1 HUMAN PRELIMINARY; PRT; 1335 AA.
AC Q86VH1
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE KIF27B.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=22730772; PubMed=12783626; DOI=10.1186/1471-2164-4-22;
RA Oduru S., Campbell J.L., Karri S., Hendry W.J., Khan S.A.,
RA Williams S.C.;
RT "Gene discovery in the hamster: a comparative genomics approach for
RT gene annotation by sequencing of hamster testis cDNAs.";
RL BMC Genomics 4:22-22(2003).
DR EMBL; AV237537; AAP04414.1; -; mRNA.
DR HSP; P33173; I15S.
DR GO; GO:0005874; C:microtubule; IEA.
DR GO; GO:0005875; C:microtubule associated complex; IEA.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0003777; F:microtubule motor activity; IEA.
DR GO; GO:0007018; P:microtubule-based movement; IEA.
DR InterPro; IPR001752; kinesin_motor.
DR Pfam; PF00225; Kinesin; 1.
DR PRINTS; PR00380; KINESINHEAVY.
DR SMART; SM00129; KISC; 1.
DR PROSITE; PS00411; KINESIN_MOTOR_DOMAIN1; UNKNOWN_1.
DR PROSITE; PS0067; KINESIN_MOTOR_DOMAIN2; 1.
KW ATP-binding; Microtubule; Motor protein; Nucleotide-binding.
SQ SEQUENCE 1335 AA; 152314 MW; D3D02A926D9E823F CRC64;

Query Match 65.8%; Score 52; DB 2; Length 1335;
Best Local Similarity 66.7%; Pred. No. 2.4;
Matches 10; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 RHYGETKNQRSRS 15
Db 193 RHTGTTQNHSSRS 207

RESULT 30
Q7M6Z5 RAT
ID Q7M6Z5 RAT PRELIMINARY; PRT; 1394 AA.
AC Q7M6Z5
DT 01-MAR-2004 (TrEMBLrel. 26, Created)
DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Kinesin-related protein KIF27A.
GN Name=LOC306736;
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP NUCLEOTIDE SEQUENCE.
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RX MEDLINE=22730772; PubMed=12783626; DOI=10.1186/1471-2164-4-22;
RA Oduru S., Campbell J.L., Karri S., Hendry W.J., Khan S.A.,
RA Williams S.C.;
RT "Gene discovery in the hamster: a comparative genomics approach for
RT gene annotation by sequencing of hamster testis cDNAs.";
RL BMC Genomics 4:22-22(2003).
CC -!- MISCELLANEOUS: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ third party annotation (TPA) entry.
DR EMBL; BK001053; DAA01311.1; -; mRNA.
DR HSP; P33173; I15S.
DR Ensembl; ENSRNOG0000019257; Rattus norvegicus.
DR RGD; 727818; LOC308736.
DR GO; GO:0005874; C:microtubule; IEA.
DR GO; GO:0005875; C:microtubule associated complex; IEA.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0003777; F:microtubule motor activity; IEA.
DR GO; GO:0007018; P:microtubule-based movement; IEA.
DR InterPro; IPR001752; kinesin_motor.
DR Pfam; PF00225; Kinesin; 1.
DR PRINTS; PR00380; KINESINHEAVY.
DR PROSITE; PS00411; KINESIN_MOTOR_DOMAIN1; UNKNOWN_1.
DR PROSITE; PS0067; KINESIN_MOTOR_DOMAIN2; 1.
KW ATP-binding; Microtubule; Motor protein; Nucleotide-binding.
SQ SEQUENCE 1394 AA; 158880 MW; 78E6AA7FF01C7987 CRC64;

Query Match 65.8%; Score 52; DB 2; Length 1394;
Best Local Similarity 66.7%; Pred. No. 2.6;
Matches 10; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 RHYGETKNQRSRS 15
Db 193 RHTGTTQNHSSRS 207

RESULT 31
Q7M6Z4 MOUSE
ID Q7M6Z4 MOUSE PRELIMINARY; PRT; 1394 AA.
AC Q7M6Z4
DT 01-MAR-2004 (TrEMBLrel. 26, Created)
DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Kinesin-related protein KIF27A.
GN Name=Kif27;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=22730772; PubMed=12783626; DOI=10.1186/1471-2164-4-22;
RA Oduru S., Campbell J.L., Karri S., Hendry W.J., Khan S.A.,
RA Williams S.C.;
RT "Gene discovery in the hamster: a comparative genomics approach for
RT gene annotation by sequencing of hamster testis cDNAs.";
RL BMC Genomics 4:22-22(2003).
CC -!- MISCELLANEOUS: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ third party annotation (TPA) entry.
DR EMBL; BK001056; DAA01314.1; -; mRNA.
DR HSP; P33173; I15S.
DR Ensembl; ENSMUSG00000060176; Mus musculus.
DR MGI; MGI:1922300; Kif27.
DR GO; GO:0005874; C:microtubule; IEA.
DR GO; GO:0005875; C:microtubule associated complex; IEA.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0003777; F:microtubule motor activity; IEA.
DR GO; GO:0007018; P:microtubule-based movement; IEA.
DR InterPro; IPR001752; kinesin_motor.
DR Pfam; PF00225; Kinesin; 1.
DR PRINTS; PR00380; KINESINHEAVY.
DR PROSITE; PS00411; KINESIN_MOTOR_DOMAIN1; UNKNOWN_1.
DR PROSITE; PS0067; KINESIN_MOTOR_DOMAIN2; 1.
KW ATP-binding; Microtubule; Motor protein; Nucleotide-binding.
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SQ SEQUENCE 1394 AA; 158956 MW; AC5F7CCD2CA61D6B CRC64;
Query Match 65.8%; Score 52; DB 2; Length 1394;
Best Local Similarity 66.7%; Pred. No. 2.6;
Matches 10; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 RHYGETKNQRRSSRS 15
|||::|:|
Db 193 RHTGTTQNHSSRS 207

RESULT 32
Q86VH2 HUMAN
ID Q86VH2_HUMAN PRELIMINARY; PRT; 1401 AA.
AC Q86VH2
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE KIF27A [OTTHUMP0000021559].
GN Name=KIF27; Synonyms=RP11-575L7.3; ORFNames=RP11-575L7.3-001;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]_TaxID=9606;
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=22730772; PubMed=12783626; DOI=10.1186/1471-2164-4-22;
RA Oduro S., Campbell J.L., Karri S., Hendry W.J., Khan S.A.,
RA Williams S.C.;
RT "Gene discovery in the hamster: a comparative genomics approach for
RT gene annotation by sequencing of hamster testis cDNAs.";
RL BMC Genomics 4:22-22(2003).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RA Beasley H.;
RL Submitted (MAY-2005) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY237536; AAP04413.1; -; mRNA.
DR EMBL; AL354733; CA116013.1; -; Genomic_DNA.
DR HSSP; P33173; 1155.
DR Ensembl; ENSG00000165115; Homo sapiens.
DR HGNC; HGNC:18632; KIF27.
DR GO; GO:0005874; C:microtubule; IEA.
DR GO; GO:0005875; C:microtubule associated complex; IEA.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0003777; F:microtubule motor activity; IEA.
DR GO; GO:0007018; P:microtubule-based movement; IEA.
DR InterPro; IPR001752; kinesin_motor.
DR Pfam; PF00225; Kinesin; 1.
DR PRINTS; PRO0380; KINESINHEAVY.
DR SMART; SM00129; KISC; 1.
DR PROSITE; PS00411; KINESIN_MOTOR_DOMAIN1; UNKNOWN_1.
DR PROSITE; PS00667; KINESIN_MOTOR_DOMAIN2; 1.
KW ATP-binding; Microtubule; Motor protein; Nucleotide-binding.
SQ SEQUENCE 1401 AA; 160283 MW; 4563BA14C30DB21 CRC64;

Query Match 65.8%; Score 52; DB 2; Length 1401;
Best Local Similarity 66.7%; Pred. No. 2.6;
Matches 10; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 RHYGETKNQRRSSRS 15
|||::|:|
Db 193 RHTGTTQNHSSRS 207

RESULT 33
Q9NCF9 DROME
ID Q9NCF9_DROME PRELIMINARY; PRT; 1931 AA.
AC Q9NCF9
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Mitotic kinesin-like motor protein CNP-ana.

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GN Name=cana; ORFNames=CG4831;
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]_TaxID=7227;
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=20351410; PubMed=10893249; DOI=10.1083/jcb.150.1.1;
RA Yucel J.K., Marszalek J.D., McIntosh J.R., Goldstein L.S.B.,
RA Cleveland D.W., Philip A.V.;
RT "CENP-meta, an essential kinetochore kinesin required for the
RT maintenance of metaphase chromosome alignment in Drosophila.";
RL J. Cell Biol. 150:1-11(2000).
DR EMBL; AF220354; AAF32356.1; -; mRNA.
DR HSSP; P17119; IF9T.
DR FlyBase; FBgn0040233; cana.
DR GO; GO:000090; P:mitotic anaphase; IMP.
DR InterPro; IPR005602; DUF334.
DR InterPro; IPR001752; kinesin_motor.
DR Pfam; PF00225; Kinesin; 1.
DR PRINTS; PRO0380; KINESINHEAVY.
DR ProDom; PD038149; DUF334; 1.
DR SMART; SM00129; KISC; 1.
DR PROSITE; PS00411; KINESIN_MOTOR_DOMAIN1; 1.
DR PROSITE; PS00667; KINESIN_MOTOR_DOMAIN2; 1.
KW ATP-binding; Microtubule; Motor protein; Nucleotide-binding.
SQ SEQUENCE 1931 AA; 221863 MW; 49984D6757588D67 CRC64;

Query Match 65.8%; Score 52; DB 2; Length 1931;
Best Local Similarity 73.3%; Pred. No. 3.8;
Matches 11; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 RHYGETKNQRRSSRS 15
|||::|:|
Db 183 RVGGETNNRSSRS 197

RESULT 34
Q9VKH9 DROME
ID Q9VKH9_DROME PRELIMINARY; PRT; 1931 AA.
AC Q9VKH9
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE CG32955-PE, isoform E.
GN Name=cana; Synonyms=CG32955; ORFNames=CG32955, CG4831;
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]_TaxID=7227;
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=20196006; PubMed=10731132; DOI=10.1126/science.287.5461.2185;
RA Adams M.D., Celnik S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Vandeil M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Abrial J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Bertram B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brotter P.,
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
RA Fowler C., Gabriellian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D.A., Heiman T.J., Hernandez J.R., Houck J.,

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DE Kinesin like protein.
GN Name=F19H22.50; Synonyms=AT938950;
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
OC rosids; eustosids II; Brassicales; Brassicaceae; Arabidopsia.
OC NCBI_TaxID=3702;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Bevan M., Murphy G., Ridley P., Hudson S., Bancroft I., Mewes H.W.,
RA Mayer K.F.X., Schueller C.;
RL Submitted (MAR-1999) to the EMBL/GenBank/DBJ databases.
RN [2]
RP NUCLEOTIDE SEQUENCE.
RA EU Arabidopsis sequencing project;
RL Submitted (MAR-1999) to the EMBL/GenBank/DBJ databases.
RN [3]
RP NUCLEOTIDE SEQUENCE.
RA Murphy G., Ridley P., Hudson S., Mewes H.W., Lemcke K., Mayer K.F.X.;
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
RN [4]
RP NUCLEOTIDE SEQUENCE.
RA EU Arabidopsis sequencing project;
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AL035679; CAB38815.1; -; Genomic DNA.
DR EMBL; AL161594; CAB80558.1; -; Genomic DNA.
DR PIR; T06055; T06055.
DR HSP; P31173; I158.
DR GO; GO:0005874; C:microtubule; IEA.
DR GO; GO:0005875; C:microtubule associated complex; IEA.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0003777; F:microtubule motor activity; IEA.
DR GO; GO:0007018; P:microtubule-based movement; IEA.
DR InterPro; IPR001752; kinesin_motor.
DR Pfam; PF00225; Kinesin; 1.
DR PRINTS; PR00380; KINESINHEAVY.
DR SMART; SM00129; KISC; 1.
DR PROSITE; PSS0067; KINESIN MOTOR DOMAIN2; 1.
SQ SEQUENCE 834 AA; 94434 MW; 0A0F1835C4544C4B CRC64;
Query Match 64.6%; Score 51; DB 2; Length 834;
Best Local Similarity 66.7%; Pred. No. 2.1;
Matches 10; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
QY 1 RHYGETQNMQRSSRS 15
DB 214 RKIGETSLNRSRS 228
RESULT 37
Q9VRK9 DROME PRELIMINARY; PRT; 677 AA.
AC Q9VRK9
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE CG10642-PA.
GN Name=Klp64D; ORFNames=CG10642;
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OC NCBI_TaxID=7227;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=20196006; PubMed=10731132; DOI=10.1126/science.287.5461.2185;
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Heit G., Nelson C.R., Miklos G.D.G.,
RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,

RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson D.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borokova D., Botchan M.R., Bouck J., Brokstein P., Brotter P.,
RA Burtis K.C., Busam D.A., Buhle H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahle C., Davenport L.B., Davies P.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferrier S., Fleischmann W.,
RA Floss C., Gabriellian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D.A., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Lasko P., Lei Y., Levitsky A.A., Li J.H., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Pacleb J.M.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusakern D.R., Pacleb J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of Drosophila melanogaster."
RL Science 287:2185-2195(2000).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=22426065; PubMed=12537568;
RA Celniker S.E., Wheeler D.A., Kronmiller B., Carlson J.W., Halpern A.,
RA Patel S., Adams M., Champe M., Dugan S.P., Frise E., Hodgson A.,
RA George R.A., Hoskins R.A., Lavery T., Muzny D.M., Nelson C.R.,
RA Pacleb J.M., Park S., Pfeiffer B.D., Richards S., Sodergren E.J.,
RA Svirskas R., Tabor P.E., Wan K., Stapleton M., Sutton G.G., Venter C.,
RA Weinstock G., Scherer S.E., Myers E.W., Gibbs R.A., Rubin G.M.;
RT "Finishing a whole-genome shotgun: release 3 of the Drosophila
melanogaster euchromatic genome sequence."
RT Genome Biol. 3:RESEARCH0079-RESEARCH0079(2002).
RN [3]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=22426070; PubMed=12537573;
RA Kaminker J.S., Bergman C.M., Kronmiller B., Carlson J.W., Svirskas R.,
RA Patel S., Frise E., Wheeler D.A., Lewis S.E., Rubin G.M.,
RA Ashburner M., Celniker S.E.;
RT "The transposable elements of the Drosophila melanogaster euchromatin:
a genomics perspective."
RT Genome Biol. 3:RESEARCH0084.1-RESEARCH0084.20(2002).
RN [4]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=22426069; PubMed=12537572;
RA Misra S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,
RA Hradecky P., Huang Y., Kaminker J.S., Millburn G.H., Prochuk S.E.,
RA Smith C.D., Tupy J.L., Whitfield E.J., Bayraktaroglu L., Berman B.P.,
RA Bettecourt B.R., Celniker S.E., de Grey A.D.N.J., Drysdale R.A.,
RA Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q.,
RA Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
RA Lewis S.E.;
RT "Annotation of the Drosophila melanogaster euchromatic genome: a
systematic review."
RT Genome Biol. 3:RESEARCH0083.1-RESEARCH0083.22(2002).
RN [5]
RP NUCLEOTIDE SEQUENCE.
RG Berkeley Drosophila Genome Project;
RA Celniker S., Carlson J., Wan K., Pfeiffer B., Frise E., George R.,
RA Hoskins R., Stapleton M., Pacleb J., Park S., Svirskas R., Smith E.,
RA Yu C., Rubin G.;
RT "Drosophila melanogaster release 4 sequence."
RT Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.


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DR PROSITE; P850067; KINESIN MOTOR DOMAIN2; 1.
KW ATP-binding; Hypothetical protein; Microtubule; Motor protein;
KW Nucleotide-binding.
SQ SEQUENCE 1043 AA; 112789 MW; F215D12A27628ACC CRC64;

Query Match 63.3%; Score 50; DB 2; Length 1043;
Best Local Similarity 66.7%; Pred. No. 4.3;
Matches 10; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 RHYGETKNQSRSS 15
DB 506 RHVGATDWNERSRS 520

RESULT 40
ID Q4PG67_USTWA PRELIMINARY; PRT; 1459 AA.
AC Q4PG67;
DT 13-SEP-2005 (TrEMBLrel. 31, Created)
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE Hypothetical protein.
GN ORFNames=UM00896.1;
OS Ustilago maydis 521.
OC Eukaryota; Fungi; Basidiomycota; Ustilaginomycetes;
OC Ustilaginomycetidae; Ustilaginales; Ustilaginaceae; Ustilago.
OX NCBI_TaxID=237631;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=521;
RA Birren B., Nusbaum C., Abebe A., Abouelleil A., Adekova E.,
RA Ait-zahra M., Allen N., Allen T., An P., Anderson M., Anderson S.,
RA Arachchi H., Armbruster J., Bachantsang P., Baldwin J., Barry A.,
RA Bayul T., Blishsteyn B., Bloom T., Blye J., Boguslavskiy L.,
RA Borowsky M., Boukhalter B., Brunache A., Butler J., Calixte N.,
RA Calvo S., Camarata J., Campo K., Chang J., Cheshatsang Y., Citroen M.,
RA Collimore A., Considine T., Cook A., Cooke P., Corum B., Cuomo C.,
RA David R., Dawoe T., Degray S., Dodge S., Dooley K., Dorje P.,
RA Dorjee K., Dorris L., Duffey N., Dupes A., Elkins T., Engels R.,
RA Erickson J., Farina A., Faro S., Ferreira P., Fischer H.,
RA Fitzgerald M., Foley K., Gage D., Galagan J., Gearin G., Gnerre S.,
RA Kellis C., Kieu A., Ksner P., Kodira C., Kulbokas E., Labutti K.,
RA Lama D., Landers T., Leger J., Levine S., Lewis D., Lewis T.,
RA Lmbdad-toh K., Liu X., Lokvitsang T., Lokvitsang Y., Lucien O.,
RA Lui A., Ma L.J., Mabbitt R., Macdonald J., Maclean C., Major J.,
RA Manning J., Marabella R., Maru K., Matthews C., Mauceli E.,
RA McCarthy M., McDonough S., Mcghee T., Meldrim J., Meneus L.,
RA Mesirov J., Mihalov A., Mihova T., Mikkelson T., Mienga V., Moru K.,
RA Mozes J., Multain L., Munson G., Naylor J., News C., Nguyen C.,
RA Nguyen N., Nguyen T., Nicol R., Nielsen C., Nizzari M., Norbu C.,
RA Norbu N., O'donnell P., Okawa O., O'leary S., Omotosho B.,
RA O'Neill K., Oman S., Parker S., Perrin D., Phunkhang P., Pignani B.,
RA Purcell S., Rachupka T., Ramasamy U., Rameau R., Ray V., Raymond C.,
RA Retta R., Richardson S., Rice C., Rodriguez J., Rogers J., Rogov P.,
RA Rutman M., Schupbach R., Seaman C., Settipalli S., Sharpe T.,
RA Sheridan J., Sherpa N., Shi J., Smirnov S., Smith C., Sougnez C.,
RA Spencer B., Stalker J., Stange-thomann N., Stavropoulos S.,
RA Stenson K., Stone C., Stone S., Stubbs M., Talamas J., Tchuinga P.,
RA Tenzing P., Tesfaye S., Theodore J., Thoulutsang Y., Topham K.,
RA Towey S., Tsamla T., Tsomo N., Vallee D., Vassiliev H.,
RA Venkataraman V., Vinson J., Vo A., Wade C., Wang S., Wangchuk T.,
RA Wangdi T., Whittaker C., Wilkinson J., Wu Y., Wyman D., Yadav S.,
RA Yang S., Yang X., Yeager S., Yee E., Young G., Zainoun J., Zembeck L.,
RA Zimmer A., Zody M., Lander E.;
RT "The genome sequence of Ustilago maydis";
RL Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.

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DR BML; AACP0100030; EAK82080.1; -, Genomic_DNA.
KW Hypothetical protein.
SQ SEQUENCE 1459 AA; 156992 MW; AC26C55B99645558 CRC64;

Query Match 63.3%; Score 50; DB 2; Length 1459;
Best Local Similarity 66.7%; Pred. No. 6.5;
Matches 10; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 RHYGETKNQSRSS 15
DB 487 RHVGATDWNERSRS 501

RESULT 41
ID P87198_USTWA PRELIMINARY; PRT; 1459 AA.
AC P87198;
DT 01-JUL-1997 (TrEMBLrel. 04, Created)
DT 01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Kinesin motor protein.
GN Name=kinl;
OS Ustilago maydis (Smut fungus).
OC Eukaryota; Fungi; Basidiomycota; Ustilaginomycetes;
OC Ustilaginomycetidae; Ustilaginales; Ustilaginaceae; Ustilago.
OX NCBI_TaxID=5270;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=97361828; PubMed=9218789; DOI=10.1093/emboj/16.12.3464;
RA Lehner C., Steinberg G., Snetelaar K.M., Schliwa M., Kahmann R.,
RA Bolker M.;
RT "Identification of a motor protein required for filamentous growth in
RT Ustilago maydis.";
RL EMBO J. 16:3464-3473(1997).
DR EMBL; U92844; AAB63336.1; -, Genomic_DNA.
DR PIR; T30196; T30196.
DR HSSP; P33173; 1I6I.
DR GO; GO:0005874; C:microtubule; IEA.
DR GO; GO:0005875; C:microtubule associated complex; IEA.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0003777; F:microtubule motor activity; IEA.
DR GO; GO:0007018; F:microtubule-based movement; IEA.
DR InterPro; IPR001752; kinesin_motor.
DR Pfam; PF00225; Kinesin; 1.
DR PRINTS; SM00380; KINESINHEAVY.
DR SMART; SM00129; KISG; 1.
DR PROSITE; PS00411; KINESIN_MOTOR_DOMAIN1; 1.
DR PROSITE; PS0067; KINESIN_MOTOR_DOMAIN2; 1.
KW ATP-binding; Microtubule; Motor protein; Nucleotide-binding.
SQ SEQUENCE 1459 AA; 156933 MW; 281B74B0100F5CD0 CRC64;

Query Match 63.3%; Score 50; DB 2; Length 1459;
Best Local Similarity 66.7%; Pred. No. 6.5;
Matches 10; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 RHYGETKNQSRSS 15
DB 487 RHVGATDWNERSRS 501

RESULT 42
Q9U679_STRPU
ID Q9U679_STRPU PRELIMINARY; PRT; 1624 AA.
AC Q9U679;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Kinesin-C.
OS Strongylocentrotus purpuratus (Purple sea urchin).
OC Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Echinozoa;
OC Echinoidea; Euechinoidea; Echinacea; Echinoida; Strongylocentrotidae;
OC Strongylocentrotus.
OX NCBI_TaxID=7668;

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[1]
RN NUCLEOTIDE SEQUENCE.
RP MEDLINE=20027084; PubMed=10556023; DOI=10.1006/jmbi.1999.3249;
RX Rogers G.C., Hart C.L., Wedaman K.P., Scholey J.M.;
RA "Identification of Kinesin-C, a calmodulin-binding carboxy-terminal
RT kinesin in animal (Strongylocentrotus purpuratus) cells.";
RL J. Mol. Biol. 294:1-8(1999).
DR EMBL; AF191095; AAF04841.1; -; mRNA.
DR HSSP; P17119; 1F9W.
DR GO; GO:0005874; C:microtubule; IEA.
DR GO; GO:0005875; C:microtubule associated complex; IEA.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0003777; F:microtubule motor activity; IEA.
DR GO; GO:0007018; P:microtubule-based movement; IEA.
DR InterPro; IPR001752; P:microtubule-based movement; IEA.
DR Pfam; PF00225; Kinesin; 1.
DR PRINTS; PR00380; KINESINHEAVY.
DR SMART; SM00129; KISC; 1.
DR PROSITE; PS00411; KINESIN_MOTOR_DOMAIN1; 1.
DR PROSITE; PS50067; KINESIN_MOTOR_DOMAIN2; 1.
KW ATP-binding; Microtubule; Motor protein; Nucleotide-binding.
SQ SEQUENCE 1624 AA; 180899 MW; AAFD758487F1B7AA CRC64;

Query Match 63.3%; Score 50; DB 2; Length 1624;
Best Local Similarity 66.7%; Pred. No. 7.4;
Matches 10; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 RHYGETKNQSSRS 15
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DB 1454 RHVASTKNSSRS 1468

RESULT 43
QI1113 MORSA
ID Q91113 MORSA PRELIMINARY; PRT; 146 AA.
AC Q91113;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-WAR-2004 (TrEMBLrel. 26, Last annotation update)
DE FKIF4 (Fragment).
GN Name=fkif4;
OS Morone saxatilis (Striped bass).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Perciformes; Percoidae;
OC Moronidae; Morone.
OX NCBI_TaxID=34816;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Retina;
RA Bost-Usinger L., Burnside B.;
RL Submitted (AUG-1995) to the EMBL/GenBank/DBJ databases.
DR EMBL; U34656; AAB03190.1; -; mRNA.
DR HSSP; P20480; IN6M.
DR GO; GO:0005874; C:microtubule associated complex; IEA.
DR GO; GO:0005875; C:microtubule associated complex; IEA.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0003777; F:microtubule motor activity; IEA.
DR GO; GO:0007018; P:microtubule-based movement; IEA.
DR InterPro; IPR001752; Kinesin_motor.
DR Pfam; PF00225; Kinesin; 1.
DR PRINTS; PR00380; KINESINHEAVY.
DR SMART; SM00129; KISC; 1.
DR PROSITE; PS50067; KINESIN_MOTOR_DOMAIN2; 1.
KW ATP-binding; Microtubule; Motor protein; Nucleotide-binding.
FT NON_TER 1
FT NON_TER 146
SQ SEQUENCE 146 AA; 16301 MW; 97D69ED068C8A8FF CRC64;

Query Match 62.0%; Score 49; DB 2; Length 146;
Best Local Similarity 60.0%; Pred. No. 0.62;
Matches 9; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 RHYGETKNQSSRS 15
||| |||| ||||
DB 1454 RHVASTKNSSRS 1468

RESULT 43
QI1113 MORSA
ID Q91113 MORSA PRELIMINARY; PRT; 146 AA.
AC Q91113;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-WAR-2004 (TrEMBLrel. 26, Last annotation update)
DE FKIF4 (Fragment).
GN Name=fkif4;
OS Morone saxatilis (Striped bass).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Perciformes; Percoidae;
OC Moronidae; Morone.
OX NCBI_TaxID=34816;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Retina;
RA Bost-Usinger L., Burnside B.;
RL Submitted (AUG-1995) to the EMBL/GenBank/DBJ databases.
DR EMBL; U34656; AAB03190.1; -; mRNA.
DR HSSP; P20480; IN6M.
DR GO; GO:0005874; C:microtubule associated complex; IEA.
DR GO; GO:0005875; C:microtubule associated complex; IEA.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0003777; F:microtubule motor activity; IEA.
DR GO; GO:0007018; P:microtubule-based movement; IEA.
DR InterPro; IPR001752; Kinesin_motor.
DR Pfam; PF00225; Kinesin; 1.
DR PRINTS; PR00380; KINESINHEAVY.
DR SMART; SM00129; KISC; 1.
DR PROSITE; PS50067; KINESIN_MOTOR_DOMAIN2; 1.
KW ATP-binding; Microtubule; Motor protein; Nucleotide-binding.
FT NON_TER 1
FT NON_TER 146
SQ SEQUENCE 146 AA; 16301 MW; 97D69ED068C8A8FF CRC64;

Query Match 62.0%; Score 49; DB 2; Length 146;
Best Local Similarity 60.0%; Pred. No. 0.62;
Matches 9; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 RHYGETKNQSSRS 15
||| |||| ||||
DB 1454 RHVASTKNSSRS 1468

RESULT 43
QI1113 MORSA
ID Q91113 MORSA PRELIMINARY; PRT; 146 AA.
AC Q91113;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-WAR-2004 (TrEMBLrel. 26, Last annotation update)
DE FKIF4 (Fragment).
GN Name=fkif4;
OS Morone saxatilis (Striped bass).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Perciformes; Percoidae;
OC Moronidae; Morone.
OX NCBI_TaxID=34816;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Retina;
RA Bost-Usinger L., Burnside B.;
RL Submitted (AUG-1995) to the EMBL/GenBank/DBJ databases.
DR EMBL; U34656; AAB03190.1; -; mRNA.
DR HSSP; P20480; IN6M.
DR GO; GO:0005874; C:microtubule associated complex; IEA.
DR GO; GO:0005875; C:microtubule associated complex; IEA.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0003777; F:microtubule motor activity; IEA.
DR GO; GO:0007018; P:microtubule-based movement; IEA.
DR InterPro; IPR001752; Kinesin_motor.
DR Pfam; PF00225; Kinesin; 1.
DR PRINTS; PR00380; KINESINHEAVY.
DR SMART; SM00129; KISC; 1.
DR PROSITE; PS50067; KINESIN_MOTOR_DOMAIN2; 1.
KW ATP-binding; Microtubule; Motor protein; Nucleotide-binding.
FT NON_TER 1
FT NON_TER 146
SQ SEQUENCE 146 AA; 16301 MW; 97D69ED068C8A8FF CRC64;

Query Match 62.0%; Score 49; DB 2; Length 148;
Best Local Similarity 66.7%; Pred. No. 0.63;
Matches 10; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 RHYGETKNQSSRS 15
||| |||| ||||
DB 101 RAVGATRLNQRSSRS 115

RESULT 45
QI5719 DICDI
ID O15719 DICDI PRELIMINARY; PRT; 156 AA.
AC O15719;
DT 01-JAN-1998 (TrEMBLrel. 05, Created)
DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
DT 01-WAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Kinesin-related protein K4 (Fragment).
OS Dictyostelium discoideum (Slime mold).
OC Eukaryota; Mycetozoa; Dictyostellida; Dictyostelium.
OX NCBI_TaxID=44689;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=AX3;
RA de Hostos E.L., McCaffrey G., Vale R.D.;
RL Submitted (JUL-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF015713; AAB66583.1; -; Genomic_DNA.
DR HSSP; P17119; 1F9V.
DR DictyBase; DB0191404; ksnD.
DR GO; GO:0005874; C:microtubule; IEA.
DR GO; GO:0005875; C:microtubule associated complex; IEA.
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DR GO:0005524; F:ATP binding; IEA.
 DR GO:0003777; F:microtubule motor activity; IEA.
 DR GO:0007018; P:microtubule-based movement; IEA.
 DR InterPro: IPR001752; Kinesin_motor.
 DR Pfam: PF00225; Kinesin; 1.
 DR PRINTS: PR00380; KINESINHEAVY.
 DR SMART: SM00129; KISC; 1.
 DR PROSITE: PS00411; KINESIN MOTOR DOMAIN1; 1.
 DR PROSITE: PS00567; KINESIN MOTOR DOMAIN2; 1.
 KW ATP-binding; Microtubule, Motor protein; Nucleotide-binding.
 FT NON TER 1
 FT 156 156
 SQ SEQUENCE 156 AA; 17628 MW; 10A413476B343CF6 CRC64;

Query Match 62.0%; Score 49; DB 2; Length 156;
 Best Local Similarity 66.7%; Pred. No. 0.67;
 Matches 10; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 RHYGETKMNQRSSRS 15
 |||||
 DB 110 RHIGSTMNDSSRS 124

RESULT 46

O84JL8 ARATH
 ID O84JL8_ARATH PRELIMINARY; PRT; 193 AA.
 AC O84JL8;
 DT 01-JUN-2003 (TrEMBLrel. 24, Created)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
 DT 01-FEB-2005 (TrEMBLrel. 29, Last annotation update)
 DE Hypothetical protein Atg04985.
 GN Name:Atg04985;
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
 OC eurosids II; Brassicales; Brassicaceae; Arabidopsi.
 OX NCBI_TaxID=3702;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RA Yamada K., Chan M.M., Chang C.H., Dale J.M., Hsuan V.W., Lee J.M.,
 RA Onodera C.S., Quach H.L., Tang C., Toriumi M., Wong C., Wu H.C.,
 RA Yu G., Yuan S., Carninci P., Chen H., Cheuk R., Hayashizaki Y.,
 RA Ishida J., Jones T., Kamiya A., Kawai J., Kim C.J., Narusaka M.,
 RA Nguyen M., Palm C.J., Sakurai T., Satou M., Seki M., Shinn P.,
 RA Southwick A., Tripp M.G., Wu T., Shinozaki K., Davis R.W., Ecker J.R.,
 RA Theologis A.;
 RL Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RA Yamada K., Chan M.M., Chang C.H., Dale J.M., Hsuan V.W., Lee J.M.,
 RA Onodera C.S., Quach H.L., Tang C., Toriumi M., Wong C., Wu H.C.,
 RA Yu G., Yuan S., Carninci P., Chen H., Cheuk R., Hayashizaki Y.,
 RA Ishida J., Jones T., Kamiya A., Kawai J., Kim C.J., Narusaka M.,
 RA Nguyen M., Palm C.J., Sakurai T., Satou M., Seki M., Shinn P.,
 RA Southwick A., Tripp M.G., Wu T., Shinozaki K., Davis R.W., Ecker J.R.,
 RA Theologis A.;
 RL Submitted (FEB-2003) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BF002973; AAO22782.1; -; mRNA.
 DR EMBL; BF004413; AAO42407.1; -; mRNA.
 KW Hypothetical protein.
 SQ SEQUENCE 193 AA; 21924 MW; 937EE9433684B3 CRC64;

Query Match 62.0%; Score 49; DB 2; Length 193;
 Best Local Similarity 72.7%; Pred. No. 0.87;
 Matches 8; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 RHYGETKMNQR 11
 |||||
 DB 68 RHYNETRINQR 78

RESULT 47

O9MAU7_ARATH

ID O9MAU7_ARATH PRELIMINARY; PRT; 198 AA.
 AC O9MAU7;
 DT 01-OCT-2000 (TrEMBLrel. 15, Created)
 DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE F13M7.2 protein.
 GN Name=F13M7.2;
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
 OC eurosids II; Brassicales; Brassicaceae; Arabidopsi.
 OX NCBI_TaxID=3702;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RA Vysotskaia V.S., Schwartz J.R., Toriumi M., Yu G., Kwan A., Liu, S.,
 RA Li J., Kremenetskaia I., Luros J., Araujo R., Au M., Breidel V.,
 RA Buehler E., Conway K., Feng J., Kim C., Kurtz D., Li Y.,
 RA Palm C., Shinn P., Sun H., Davis R., Ecker J., Federspiel N.,
 RA Theologis A.;
 RL Submitted (AUG-1998) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RA Theologis;
 RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AC004809; AAF40462.1; -; Genomic_DNA.
 DR F1R; B86183; B86183.
 SQ SEQUENCE 198 AA; 22437 MW; 7BBAAB2E089F9D82 CRC64;
 Query Match 62.0%; Score 49; DB 2; Length 198;
 Best Local Similarity 72.7%; Pred. No. 0.9;
 Matches 8; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
 QY 1 RHYGETKMNQR 11
 |||||
 DB 73 RHYNETRINQR 83

RESULT 48
 Q4SIJ2_TETNG
 ID Q4SIJ2_TETNG PRELIMINARY; PRT; 573 AA.
 AC Q4SIJ2;
 DT 13-SEP-2005 (TrEMBLrel. 31, Created)
 DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
 DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
 DE Chromosome 5 SCAP14581, whole genome shotgun sequence.
 DE (Fragment).
 ORFNames=GSTENG00017667001;
 OS Tetraodon nigroviridis (Green puffer).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
 OC Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
 OC Tetraodontidae; Tetraodontidae; Tetraodon.
 OX NCBI_TaxID=99883;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RA Jaillon O., Aury J.M., Brunet F., Petit J.L., Stange-Thomann N.,
 RA Mauceli E., Bouneau L., Fischer C., Ozouf-Costaz C., Bernot A.,
 RA Nicaud S., Jaffe D., Fisher S., Lutfalla G., Dossat C., Segurens B.,
 RA Dasilva C., Salanoubat M., Levy M., Boudet N., Castellano S.,
 RA Anthouard V., Jubin C., Castelli V., Katinka M., Vacherie B.,
 RA Biemont C., Skallii Z., Cattolico L., Poulsen J., De Berardinis V.,
 RA Craud C., Duprat S., Brottier P., Coutanceau J.P., Guzy J.,
 RA Parra G., Lardier G., Chapelle C., McKernan K.J., McEwan P., Bosak S.,
 RA Kellis M., Wolff J.N., Guigo R., Zody M.C., Mesirov J.,
 RA Lindblad-Toh K., Birren B., Nusbaum C., Kahn D., Robinson-Rechavi M.,
 RA Laudet V., Schachter V., Quetier F., Saurin W., Scarpelli C.,
 RA Wincker P., Lander E.S., Weissenbach J., Roest Crolius H.;
 RT "Genome duplication in the teleost fish Tetraodon nigroviridis reveals
 RT the early vertebrate proto-karyotype.";
 RN Nature 431:946-957(2004).
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RP Genoscope; Whitehead Institute Centre for Genome Research;

RL Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL; CAAG01014581; CAF99540.1; -; Genomic_DNA.
DR InterPro; IPR001752; kinesin_motor.
DR Pfam; PF00225; Kinesin; 1.
DR PRINTS; PR00380; KINESINHEAVY.
DR SMART; SM00129; KISC; 1.
DR PROSITE; PS00411; KINESIN_MOTOR_DOMAIN1; UNKNOWN_1.
DR PROSITE; PS00067; KINESIN_MOTOR_DOMAIN2; 1.
KW ATP-binding; Microtubule; Motor protein; Nucleotide-binding.
FT NON_TER 573 573
SQ SEQUENCE 573 AA; 63898 MW; 35922F1E0A592BBA CRC64;

Query Match 62.0%; Score 49; DB 2; Length 573;
Best Local Similarity 66.7%; Pred. No. 3.2;
Matches 10; Conservative 1; Mismatches 4; Indels 0; Gaps 0;
Qy 1 RHYGETKNQSRSS 15
Db 313 RHTGATQNPNSRS 327
||| |::||| |

RESULT 49
QSR9A3_PONPY
ID Q5R9A3_PONPY PRELIMINARY; PRT; 597 AA.
AC Q5R9A3
DT 01-FEB-2005 (TREMBlrel. 29, Created)
DT 01-FEB-2005 (TREMBlrel. 29, Last sequence update)
DT 01-FEB-2005 (TREMBlrel. 29, Last annotation update)
DE Hypothetical protein DKFZp459I1739.
GN Name=DKFZp459I1739;
OS Pongo pygmaeus (Orangutan).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Pongo.
OX NCBI_TaxID=9600;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Cortex.
RG The German cDNA Consortium;
RA Koehrer K., Beyer A., Mewes H.W., Weil B., Amid C., Osanger A.,
RA Fobo G., Han M., Wiemann S.;
RL Submitted (NOV-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; CR859487; CAH91657.1; -; mRNA.
DR GO; GO:0005622; C:intracellular; IEA.
DR GO; GO:0005874; C:microtubule; IEA.
DR GO; GO:0005875; C:microtubule associated complex; IEA.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0003677; F:DNA binding; IEA.
DR GO; GO:0003777; F:microtubule motor activity; IEA.
DR GO; GO:0007018; F:microtubule-based movement; IEA.
DR InterPro; IPR003583; HHH1_Bd.
DR InterPro; IPR001752; kinesin_motor.
DR Pfam; PF00225; Kinesin; 1.
DR PRINTS; PR00380; KINESINHEAVY.
DR SMART; SM00278; Hhh1; 2.
DR SMART; SM00129; KISC; 1.
DR PROSITE; PS00411; KINESIN_MOTOR_DOMAIN1; 1.
DR PROSITE; PS00067; KINESIN_MOTOR_DOMAIN2; 1.
KW ATP-binding; Hypothetical protein; Microtubule; Motor protein;
KW Nucleotide-binding.
SQ SEQUENCE 597 AA; 66332 MW; 3F1A83D8C86F12B3 CRC64;

Query Match 62.0%; Score 49; DB 2; Length 597;
Best Local Similarity 66.7%; Pred. No. 3.4;
Matches 10; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
Qy 1 RHYGETKNQSRSS 15
Db 164 RTVGATRLNQSRSS 178
||| |::||| |

RESULT 50
Q4R838_MACFA
ID Q4R838_MACFA PRELIMINARY; PRT; 600 AA.
AC Q4R838
DT 13-SEP-2005 (TREMBlrel. 31, Created)
DT 13-SEP-2005 (TREMBlrel. 31, Last sequence update)
DT 13-SEP-2005 (TREMBlrel. 31, Last annotation update)
DE Testis cDNA clone: QtsA-13558, similar to human kinesin family member
DE 22 (KIF22).
OS Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
OC Cercopitheidae; Cercopitheciinae; Macaca.
OX NCBI_TaxID=9541;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RG International consortium for macaque cDNA sequencing, analysis;
RA "DNA sequences of macaque genes expressed in brain or testis and its
RT evolutionary implications.";
RL Submitted (JUN-2005) to the EMBL/GenBank/DBJ databases.
RN [2]
RP NUCLEOTIDE SEQUENCE.
RA Osada N., Hirata M., Tanuma R., Kusuda J., Hida M., Suzuki Y.,
RA Sugano S., Gojobori T., Shen J.C.-K., Wu C.I., Hashimoto K.;
RT "Substitution rate and structural divergence of 5'UTR evolution:
RT Comparative analysis between human and cynomolgus monkey cDNAs.";
RL Submitted (MAR-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB168622; BAB00734.1; -; mRNA.
DR InterPro; IPR003583; HHH1_Bd.
DR InterPro; IPR001752; kinesin_motor.
DR Pfam; PF00225; Kinesin; 1.
DR PRINTS; PR00380; KINESINHEAVY.
DR SMART; SM00278; Hhh1; 2.
DR SMART; SM00129; KISC; 1.
DR PROSITE; PS00411; KINESIN_MOTOR_DOMAIN1; 1.
DR PROSITE; PS00067; KINESIN_MOTOR_DOMAIN2; 1.
KW ATP-binding; Microtubule; Motor protein; Nucleotide-binding.
SQ SEQUENCE 600 AA; 66659 MW; 54D9132DFD291FF5 CRC64;

Query Match 62.0%; Score 49; DB 2; Length 600;
Best Local Similarity 66.7%; Pred. No. 3.4;
Matches 10; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
Qy 1 RHYGETKNQSRSS 15
Db 164 RTVGATRLNQSRSS 178
||| |::||| |

Search completed: April 21, 2006, 13:41:59
Job time : 260 secs

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: April 21, 2006, 13:42:16 ; Search time 47 Seconds
(without alignments)
26.386 Million cell updates/sec

Title: US-09-993-399-1

Perfect score: 79

Sequence: 1 RHYGETKNQSRSSRS 15

Scoring table: BLOSOM62

Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1000 summaries

Database : Issued Patents AA:*

1: /cgn2_6/ptodata/1/iaa/5 COMB.pep.*

2: /cgn2_6/ptodata/1/iaa/6 COMB.pep.*

3: /cgn2_6/ptodata/1/iaa/H COMB.pep.*

4: /cgn2_6/ptodata/1/iaa/PCTUS COMB.pep.*

5: /cgn2_6/ptodata/1/iaa/RE COMB.pep.*

6: /cgn2_6/ptodata/1/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	79	100.0	2662	2	US-09-595-684B-31
2	79	100.0	2663	2	US-09-538-092-1252
3	69	87.3	2354	2	US-09-150-867-1
4	54	68.4	955	1	US-08-006-676B-1
5	54	68.4	955	1	US-08-282-845-2
6	54	68.4	955	1	US-08-428-414A-3
7	54	68.4	955	4	PCT-US94-00324-1
8	52	65.8	341	2	US-09-724-517-4
9	52	65.8	341	2	US-09-641-807A-4
10	52	65.8	341	2	US-09-723-096-4
11	52	65.8	1279	2	US-09-724-517-2
12	52	65.8	1279	2	US-09-641-807A-2
13	52	65.8	1279	2	US-09-723-096-2
14	49	62.0	346	2	US-09-724-224-6
15	49	62.0	346	2	US-10-093-317-6
16	49	62.0	370	2	US-09-724-224-2
17	49	62.0	370	2	US-10-093-317-2
18	49	62.0	487	2	US-09-724-224-8
19	49	62.0	487	2	US-10-093-317-8
20	49	62.0	490	2	US-09-949-016-8784
21	49	62.0	512	2	US-09-724-224-4
22	49	62.0	512	2	US-10-093-317-4
23	49	62.0	665	2	US-09-595-684B-35
24	48	60.8	324	2	US-09-183-861-53
25	48	60.8	324	2	US-09-022-765-53
26	48	60.8	324	2	US-09-551-974A-53
27	48	60.8	324	2	US-09-565-501A-53

28	48	60.8	324	2	US-09-639-206A-53	Sequence 53, Appl
29	48	60.8	324	2	US-09-874-923-53	Sequence 53, Appl
30	45	57.0	411	1	US-08-713-815A-4	Sequence 4, Appl
31	45	57.0	441	1	US-08-713-815A-3	Sequence 3, Appl
32	45	57.0	915	2	US-09-949-016-7425	Sequence 7425, Ap
33	45	57.0	956	2	US-09-914-259-17	Sequence 17, Appl
34	45	57.0	957	2	US-09-914-259-16	Sequence 16, Appl
35	45	57.0	963	2	US-09-914-259-20	Sequence 20, Appl
36	45	57.0	963	2	US-09-914-259-22	Sequence 22, Appl
37	45	57.0	963	2	US-09-538-092-1060	Sequence 1060, Ap
38	45	57.0	967	2	US-09-914-259-21	Sequence 21, Appl
39	45	57.0	975	2	US-09-914-259-19	Sequence 19, Appl
40	45	57.0	978	2	US-09-949-016-10196	Sequence 10196, A
41	45	57.0	1027	2	US-09-914-259-27	Sequence 27, Appl
42	45	57.0	1031	2	US-09-914-259-24	Sequence 24, Appl
43	45	57.0	1032	2	US-09-914-259-26	Sequence 26, Appl
44	45	57.0	1032	2	US-09-538-092-1293	Sequence 1293, Ap
45	44	55.7	683	2	US-09-252-991A-26189	Sequence 26189, A
46	44	55.7	706	2	US-09-914-259-29	Sequence 29, Appl
47	43	54.4	337	2	US-08-641-806-4	Sequence 4, Appl
48	43	54.4	337	2	US-09-723-129-4	Sequence 4, Appl
49	43	54.4	337	2	US-09-722-862-4	Sequence 4, Appl
50	43	54.4	342	2	US-09-641-806-2	Sequence 2, Appl
51	43	54.4	342	2	US-09-723-129-2	Sequence 2, Appl
52	43	54.4	342	2	US-09-722-862-2	Sequence 2, Appl
53	43	54.4	422	2	US-09-949-016-7927	Sequence 7927, Ap
54	43	54.4	747	2	US-09-949-016-6552	Sequence 6552, Ap
55	43	54.4	760	2	US-09-949-016-10413	Sequence 10413, A
56	42	53.2	309	2	US-09-270-767-45536	Sequence 45536, A
57	42	53.2	326	2	US-09-721-383-4	Sequence 4, Appl
58	42	53.2	326	2	US-09-721-137-4	Sequence 4, Appl
59	42	53.2	326	2	US-09-721-251-4	Sequence 4, Appl
60	42	53.2	326	2	US-10-114-764-4	Sequence 4, Appl
61	42	53.2	787	2	US-09-721-383-2	Sequence 2, Appl
62	42	53.2	787	2	US-09-721-137-2	Sequence 2, Appl
63	42	53.2	787	2	US-09-721-251-2	Sequence 2, Appl
64	42	53.2	787	2	US-10-114-764-2	Sequence 2, Appl
65	41	51.9	175	2	US-08-898-659-17	Sequence 17, Appl
66	40	50.6	205	2	US-09-637-481-2	Sequence 2, Appl
67	40	50.6	205	2	US-09-723-428-2	Sequence 2, Appl
68	40	50.6	205	2	US-09-724-520-2	Sequence 2, Appl
69	39	49.4	225	2	US-09-949-016-6768	Sequence 6768, Ap
70	39	49.4	292	2	US-09-949-016-5943	Sequence 5943, Ap
71	39	49.4	321	2	US-09-949-016-11603	Sequence 11603, A
72	39	49.4	321	2	US-09-949-016-11604	Sequence 11604, A
73	39	49.4	435	2	US-09-252-991A-24914	Sequence 24914, A
74	39	49.4	499	2	US-09-248-796A-18810	Sequence 18810, A
75	39	49.4	792	2	US-09-949-016-6199	Sequence 6199, Ap
76	39	49.4	811	2	US-08-949-016-7422	Sequence 7422, Ap
77	39	49.4	884	2	US-09-741-150-4	Sequence 4, Appl
78	39	49.4	884	2	US-10-160-187-4	Sequence 4, Appl
79	39	49.4	928	2	US-09-914-259-23	Sequence 23, Appl
80	39	49.4	1038	2	US-09-541-782-4	Sequence 4, Appl
81	39	49.4	1038	2	US-09-723-820-4	Sequence 4, Appl
82	39	49.4	1038	2	US-10-270-085-4	Sequence 4, Appl
83	38	48.1	190	2	US-09-949-016-6305	Sequence 6305, Ap
84	38	48.1	331	2	US-09-949-016-6769	Sequence 6769, Ap
85	38	48.1	375	2	US-09-572-191-4	Sequence 4, Appl
86	38	48.1	375	2	US-09-723-262-4	Sequence 4, Appl
87	38	48.1	375	2	US-09-723-219-4	Sequence 4, Appl
88	38	48.1	409	2	US-09-572-191-6	Sequence 6, Appl
89	38	48.1	409	2	US-09-723-262-6	Sequence 6, Appl
90	38	48.1	409	2	US-09-723-219-6	Sequence 6, Appl
91	38	48.1	590	2	US-09-252-991A-28989	Sequence 28989, A
92	38	48.1	880	2	US-09-949-016-7110	Sequence 7110, Ap
93	38	48.1	1388	2	US-09-572-191-2	Sequence 2, Appl
94	38	48.1	1388	2	US-09-723-262-2	Sequence 2, Appl
95	38	48.1	1388	2	US-09-723-219-2	Sequence 2, Appl
96	37	46.8	130	2	US-09-270-767-33516	Sequence 33516, A
97	37	46.8	130	2	US-09-270-767-48733	Sequence 48733, A
98	37	46.8	137	2	US-08-782-480-3	Sequence 3, Appl
99	37	46.8	137	2	US-08-954-211-3	Sequence 3, Appl
100	37	46.8	137	2	US-09-005-167A-3	Sequence 3, Appl

101	37	46.8	137	2	US-09-176-741B-3	Sequence 3, Appli	174	35	44.3	660	2	US-09-786-240-10	Sequence 10, Appl
102	37	46.8	159	1	US-08-642-406A-26	Sequence 26, Appl	175	35	44.3	660	2	US-10-012-231A-88	Sequence 88, Appl
103	37	46.8	159	2	US-09-199-534-26	Sequence 26, Appl	176	35	44.3	660	2	US-10-015-389A-88	Sequence 88, Appl
104	37	46.8	159	2	US-09-199-534-26	Sequence 26, Appl	177	35	44.3	660	2	US-10-006-768A-88	Sequence 88, Appl
105	37	46.8	159	2	US-09-491-322-26	Sequence 26, Appl	178	35	44.3	660	2	US-10-015-671A-88	Sequence 88, Appl
106	37	46.8	265	2	US-09-248-796A-16478	Sequence 16478, A	179	35	44.3	660	2	US-10-011-833A-88	Sequence 88, Appl
107	37	46.8	308	2	US-09-248-796A-20449	Sequence 20449, A	180	35	44.3	660	2	US-10-006-041A-88	Sequence 88, Appl
108	37	46.8	311	2	US-09-248-796A-16958	Sequence 16958, A	181	35	44.3	660	2	US-10-012-064A-88	Sequence 88, Appl
109	37	46.8	457	2	US-09-902-540-11961	Sequence 11961, A	182	35	44.3	660	2	US-10-101-464A-891	Sequence 891, App
110	37	46.8	563	2	US-09-248-796A-18632	Sequence 18632, A	183	35	44.3	677	2	US-09-595-684B-25	Sequence 25, Appl
111	37	46.8	578	2	US-09-489-039A-10599	Sequence 10599, A	184	35	44.3	678	2	US-09-949-016-11444	Sequence 11444, A
112	37	46.8	627	2	US-09-360-545-32	Sequence 32, Appl	185	35	44.3	706	2	US-09-724-586A-1	Sequence 1, Appli
113	37	46.8	694	2	US-09-270-767-36948	Sequence 36948, A	186	35	44.3	784	2	US-09-600-823-1	Sequence 1, Appli
114	37	46.8	694	2	US-09-270-767-52165	Sequence 52165, A	187	35	44.3	784	2	US-09-724-666-1	Sequence 1, Appli
115	37	46.8	705	2	US-09-270-767-44461	Sequence 44461, A	188	35	44.3	784	2	US-09-914-259-18	Sequence 18, Appl
116	37	46.8	810	2	US-09-538-092-1275	Sequence 1275, Ap	189	35	44.3	815	2	US-09-252-991A-32759	Sequence 32759, A
117	37	46.8	1474	2	US-09-677-046A-4	Sequence 4, Appli	190	35	44.3	922	2	US-09-162-373-1	Sequence 1, Appli
118	37	46.8	1503	2	US-09-677-046A-6	Sequence 6, Appli	191	35	44.3	959	2	US-09-467-946-1	Sequence 1, Appli
119	37	46.8	1509	2	US-09-677-046A-2	Sequence 2, Appli	192	35	44.3	1103	2	US-09-949-016-9935	Sequence 9935, A
120	36	45.6	61	2	US-09-513-999C-4208	Sequence 4208, Ap	193	35	44.3	1123	2	US-09-270-767-46552	Sequence 46552, A
121	36	45.6	79	2	US-09-134-001C-3147	Sequence 3147, Ap	194	35	44.3	1123	2	US-09-595-684B-23	Sequence 23, Appl
122	36	45.6	116	2	US-09-270-767-32936	Sequence 32936, A	195	35	44.3	1231	2	US-09-592-054-2	Sequence 2, Appli
123	36	45.6	116	2	US-09-270-767-48153	Sequence 48153, A	196	35	44.3	1231	2	US-09-592-054-8	Sequence 8, Appli
124	36	45.6	168	2	US-08-990-791-10	Sequence 10, Appl	197	35	44.3	1232	2	US-09-792-616-3	Sequence 3, Appli
125	36	45.6	168	2	US-09-372-591-10	Sequence 10, Appl	198	35	44.3	1232	2	US-09-647-140B-8	Sequence 8, Appli
126	36	45.6	188	2	US-09-489-039A-14007	Sequence 14007, A	199	35	44.3	1503	2	US-09-595-684B-39	Sequence 39, Appl
127	36	45.6	248	2	US-09-050-739-60	Sequence 60, Appl	200	35	44.3	1690	2	US-09-949-016-6474	Sequence 6474, Ap
128	36	45.6	361	2	US-09-596-541-2	Sequence 2, Appli	201	35	44.3	1690	2	US-09-949-016-9887	Sequence 9887, Ap
129	36	45.6	361	2	US-10-126-205-2	Sequence 2, Appli	202	35	44.3	1695	2	US-09-513-278-5	Sequence 5, Appli
130	36	45.6	361	2	US-09-596-541-6	Sequence 6, Appli	203	34	43.0	38	1	5514582-5	Patent No. 5514582
131	36	45.6	369	2	US-09-723-595-6	Sequence 6, Appli	204	34	43.0	38	6	5514582-5	Patent No. 5514582
132	36	45.6	369	2	US-10-126-205-6	Sequence 6, Appli	205	34	43.0	89	2	US-09-252-991A-25128	Patent No. 5514582
133	36	45.6	369	2	US-09-596-541-4	Sequence 4, Appli	206	34	43.0	117	6	5514582-7	Patent No. 5514582
134	36	45.6	370	2	US-09-723-595-4	Sequence 4, Appli	207	34	43.0	117	6	5514582-7	Patent No. 5514582
135	36	45.6	370	2	US-10-126-205-4	Sequence 4, Appli	208	34	43.0	119	1	US-08-340-539A-12	Sequence 12, Appl
136	36	45.6	384	1	US-07-783-706-2	Sequence 2, Appli	209	34	43.0	140	2	US-09-645-415A-60	Sequence 60, Appl
137	36	45.6	384	1	US-08-445-342A-2	Sequence 2, Appli	210	34	43.0	156	2	US-09-543-681A-6616	Sequence 6616, Ap
138	36	45.6	384	2	US-09-066-481-2	Sequence 2, Appli	211	34	43.0	164	2	US-09-270-767-40899	Sequence 40899, A
139	36	45.6	384	2	US-09-802-285-2	Sequence 2, Appli	212	34	43.0	164	2	US-09-270-767-56115	Sequence 56115, A
140	36	45.6	384	4	PCT-US92-09124-2	Sequence 37, Appl	213	34	43.0	233	2	US-09-543-681A-5936	Sequence 5936, Ap
141	36	45.6	384	4	PCT-US92-09124-2	Sequence 37, Appl	214	34	43.0	244	2	US-09-248-796A-16447	Sequence 16447, A
142	36	45.6	519	2	US-09-595-684B-37	Sequence 10535, A	215	34	43.0	254	2	US-09-489-039A-10109	Sequence 10109, A
143	36	45.6	1437	2	US-09-949-016-10535	Sequence 6899, Ap	216	34	43.0	342	2	US-09-252-991A-24027	Sequence 24027, A
144	36	45.6	1780	2	US-09-949-016-6899	Sequence 6899, Ap	217	34	43.0	366	2	US-09-718-692-4	Sequence 4, Appli
145	36	45.6	1786	2	US-09-949-016-7880	Sequence 7880, Ap	218	34	43.0	366	2	US-09-718-852-4	Sequence 4, Appli
146	35	44.3	11	1	US-08-245-853-22	Sequence 22, Appl	219	34	43.0	366	2	US-09-513-278-4	Sequence 4, Appli
147	35	44.3	11	1	US-08-573-675-22	Sequence 22, Appl	220	34	43.0	372	1	5514582-4	Patent No. 5514582
148	35	44.3	101	2	US-09-248-796A-27613	Sequence 27613, A	221	34	43.0	372	6	5514582-4	Patent No. 5514582
149	35	44.3	119	1	US-08-340-539A-13	Sequence 13, Appl	222	34	43.0	406	2	US-09-248-796A-16921	Sequence 16921, A
150	35	44.3	137	2	US-10-101-464A-669	Sequence 669, App	223	34	43.0	421	2	US-09-107-532A-4030	Sequence 4030, Ap
151	35	44.3	137	2	US-09-270-767-32145	Sequence 32145, A	224	34	43.0	433	2	US-09-595-424-2	Sequence 2, Appli
152	35	44.3	143	2	US-09-270-767-47362	Sequence 47362, A	225	34	43.0	494	2	US-09-595-424-4	Sequence 4, Appli
153	35	44.3	167	2	US-09-270-767-46036	Sequence 46036, A	226	34	43.0	510	2	US-09-993-777-3	Sequence 3, Appli
154	35	44.3	194	2	US-09-774-639-242	Sequence 242, App	227	34	43.0	510	4	PCT-US96-03916-3	Sequence 3, Appli
155	35	44.3	260	2	US-09-270-767-41775	Sequence 41775, A	228	34	43.0	532	2	US-09-543-681A-4646	Sequence 4646, Ap
156	35	44.3	275	2	US-09-328-352-7814	Sequence 7814, Ap	229	34	43.0	560	2	US-09-270-767-44751	Sequence 44751, A
157	35	44.3	278	2	US-09-270-767-45313	Sequence 45313, A	230	34	43.0	597	2	US-09-107-532A-7053	Sequence 7053, Ap
158	35	44.3	299	2	US-09-248-796A-17636	Sequence 17636, A	231	34	43.0	611	2	US-09-902-540-14644	Sequence 14644, A
159	35	44.3	325	2	US-08-311-731A-249	Sequence 249, App	232	34	43.0	623	4	US-09-993-777-64	Sequence 64, Appl
160	35	44.3	340	2	US-09-142-593-1	Sequence 1, Appli	233	34	43.0	623	4	PCT-US96-03916-64	Sequence 64, Appl
161	35	44.3	340	2	US-09-927-886-1	Sequence 1, Appli	234	34	43.0	627	2	US-10-222-100-3	Sequence 3, Appli
162	35	44.3	404	2	US-09-328-352-6480	Sequence 6480, Ap	235	34	43.0	658	2	US-09-595-424-6	Sequence 6, Appli
163	35	44.3	412	2	US-09-347-801-21	Sequence 21, Appl	236	34	43.0	670	1	US-08-366-547-2	Sequence 2, Appli
164	35	44.3	412	2	US-09-854-731-21	Sequence 21, Appl	237	34	43.0	670	2	US-09-292-858B-2	Sequence 2, Appli
165	35	44.3	435	2	US-09-489-039A-9982	Sequence 9982, Ap	238	34	43.0	680	2	US-09-949-016-10119	Sequence 10119, A
166	35	44.3	473	2	US-09-592-054-6	Sequence 6, Appli	239	34	43.0	768	2	US-09-134-000C-6467	Sequence 6467, Ap
167	35	44.3	502	2	US-09-248-796A-16824	Sequence 16824, A	240	34	43.0	798	2	US-10-104-047-3335	Sequence 3335, Ap
168	35	44.3	522	2	US-09-592-054-4	Sequence 4, Appli	241	34	43.0	856	2	US-09-949-016-6558	Sequence 6558, Ap
169	35	44.3	632	2	US-09-976-594-41	Sequence 41, Appl	242	34	43.0	874	2	US-09-369-364A-15	Sequence 15, Appl
170	35	44.3	632	2	US-09-991-181-219	Sequence 219, App	243	34	43.0	884	2	US-09-949-016-10588	Sequence 10588, A
171	35	44.3	632	2	US-09-990-444-219	Sequence 219, App	244	34	43.0	895	2	US-09-489-039A-12499	Sequence 12499, A
172	35	44.3	632	2	US-09-997-333-219	Sequence 219, App	245	34	43.0	952	2	US-09-328-352-4551	Sequence 4551, Ap
173	35	44.3	632	2	US-09-992-598-219	Sequence 219, App	246	34	43.0	957	2	US-09-595-684B-27	Sequence 27, Appl

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248	34	43.0	1564	2	US-10-144-198-2	Sequence 2, Appli	Sequence 4, Appli	321	33	41.8	604	2	US-08-487-744-5	Sequence 5, Appli
249	34	43.0	1564	2	US-10-144-198-4	Sequence 4, Appli	Sequence 2, Appli	322	33	41.8	604	2	US-08-930-589A-18	Sequence 18, Appl
250	34	43.0	1637	2	US-09-718-852-2	Sequence 2, Appli	Sequence 2, Appli	323	33	41.8	604	2	US-09-599-781-18	Sequence 18, Appl
251	34	43.0	1637	2	US-09-718-852-2	Sequence 2, Appli	Sequence 2, Appli	324	33	41.8	604	2	US-10-027-961A-18	Sequence 18, Appl
252	34	43.0	1637	2	US-09-718-815-2	Sequence 2, Appli	Sequence 2, Appli	325	33	41.8	604	4	PCT-US93-09167-4	Sequence 4, Appli
253	34	43.0	2318	2	US-09-091-219-24	Sequence 24, Appl	Sequence 24, Appl	326	33	41.8	604	4	PCT-US93-09167-5	Sequence 5, Appli
254	34	43.0	2318	2	US-09-660-541-24	Sequence 24, Appl	Sequence 24, Appl	327	33	41.8	610	2	US-09-902-540-13312	Sequence 13312, A
255	34	43.0	2465	1	US-08-596-291-3	Sequence 3, Appli	Sequence 3, Appli	328	33	41.8	632	2	US-09-205-658-150	Sequence 150, App
256	34	43.0	2465	2	US-09-100-804-3	Sequence 3, Appli	Sequence 3, Appli	329	33	41.8	632	2	US-09-205-658-150	Sequence 150, App
257	34	43.0	2466	2	US-09-080-855-12	Sequence 12, Appl	Sequence 12, Appl	330	33	41.8	632	2	US-09-248-796A-19238	Sequence 19238, A
258	34	43.0	2466	2	US-09-566-076-12	Sequence 12, Appl	Sequence 12, Appl	331	33	41.8	623	2	US-09-594-669-14	Sequence 14, Appl
259	34	43.0	2466	4	PCT-US94-09943-2	Sequence 2, Appli	Sequence 2, Appli	332	33	41.8	723	2	US-10-112-432-14	Sequence 14, Appl
260	34	43.0	2485	2	US-09-290-640-46	Sequence 46, Appl	Sequence 46, Appl	333	33	41.8	723	2	US-09-594-669-16	Sequence 16, Appl
261	34	43.0	2485	2	US-09-665-615B-46	Sequence 46, Appl	Sequence 46, Appl	334	33	41.8	725	2	US-09-595-684B-33	Sequence 33, Appl
262	33.5	42.4	117	1	US-08-274-661B-38	Sequence 38, Appl	Sequence 38, Appl	335	33	41.8	725	2	US-10-112-432-16	Sequence 16, Appl
263	33.5	42.4	367	2	US-09-248-796A-20601	Sequence 20601, A	Sequence 20601, A	336	33	41.8	725	2	US-09-849-602-20	Sequence 20, Appl
264	33.5	42.4	372	1	US-08-513-278-2	Sequence 2, Appli	Sequence 2, Appli	337	33	41.8	867	2	US-10-197-220-109	Sequence 109, App
265	33.5	42.4	372	6	5514582-2	Patent No. 5514582	Patent No. 5514582	338	33	41.8	922	2	US-10-104-047-2694	Sequence 2694, Ap
266	33.5	42.4	385	1	US-08-340-539A-2	Sequence 2, Appli	Sequence 2, Appli	339	33	41.8	1073	2	US-09-541-782-6	Sequence 6, Appli
267	33.5	42.4	385	1	US-08-461-592B-2	Sequence 2, Appli	Sequence 2, Appli	340	33	41.8	1073	2	US-09-723-820-6	Sequence 6, Appli
268	33.5	42.4	715	2	US-09-248-796A-20602	Sequence 20602, A	Sequence 20602, A	341	33	41.8	1073	2	US-10-270-085-6	Sequence 6, Appli
269	33.5	42.4	848	2	US-09-538-092-33	Sequence 33, Appl	Sequence 33, Appl	342	33	41.8	1184	2	US-09-541-782-2	Sequence 2, Appli
270	33	41.8	23	2	US-09-537-226-13	Sequence 13, Appl	Sequence 13, Appl	343	33	41.8	1184	2	US-09-723-820-2	Sequence 2, Appli
271	33	41.8	26	1	US-08-482-142-22	Sequence 22, Appl	Sequence 22, Appl	344	33	41.8	1184	2	US-10-270-085-2	Sequence 2, Appli
272	33	41.8	26	1	US-08-478-572-22	Sequence 22, Appl	Sequence 22, Appl	345	33	41.8	1255	2	US-09-248-796A-14158	Sequence 14158, A
273	33	41.8	26	2	US-08-484-296-22	Sequence 22, Appl	Sequence 22, Appl	346	33	41.8	10182	2	US-09-134-001C-3159	Sequence 3159, Ap
274	33	41.8	81	2	US-09-537-226-16	Sequence 16, Appl	Sequence 16, Appl	347	32.5	41.1	111	2	US-09-252-991A-26279	Sequence 26279, A
275	33	41.8	90	2	US-09-809-665A-147	Sequence 147, App	Sequence 147, App	348	32.5	41.1	122	2	US-09-248-796A-22797	Sequence 22797, A
276	33	41.8	120	2	US-09-489-039A-12045	Sequence 12045, A	Sequence 12045, A	349	32.5	41.1	122	2	US-09-248-796A-23030	Sequence 23030, A
277	33	41.8	187	2	US-09-270-767-34993	Sequence 34993, A	Sequence 34993, A	350	32.5	41.1	338	2	US-09-902-540-16254	Sequence 16254, A
278	33	41.8	188	2	US-09-270-767-34999	Sequence 34999, A	Sequence 34999, A	351	32.5	41.1	463	2	US-09-543-681A-6745	Sequence 6745, Ap
279	33	41.8	188	2	US-09-270-767-34999	Sequence 34999, A	Sequence 34999, A	352	32.5	41.1	5588	2	US-09-036-987A-6	Sequence 6, Appli
280	33	41.8	245	2	US-09-252-991A-26889	Sequence 26889, A	Sequence 26889, A	353	32.5	41.1	5588	2	US-09-370-700-6	Sequence 6, Appli
281	33	41.8	254	2	US-09-328-352-5775	Sequence 30975, A	Sequence 30975, A	354	32.5	41.1	5588	1	US-09-603-207-6	Sequence 6, Appli
282	33	41.8	259	2	US-08-663-831-2	Sequence 2, Appli	Sequence 2, Appli	355	32	40.5	16	4	PCT-US96-01314-31	Sequence 31, Appl
283	33	41.8	260	2	US-09-248-796A-20535	Sequence 20535, A	Sequence 20535, A	356	32	40.5	16	4	PCT-US96-01314-31	Sequence 31, Appl
284	33	41.8	270	2	US-09-489-039A-10186	Sequence 10186, A	Sequence 10186, A	357	32	40.5	56	2	US-09-556-609C-6647	Sequence 6647, Ap
285	33	41.8	284	2	US-09-252-991A-22267	Sequence 22267, A	Sequence 22267, A	358	32	40.5	56	2	US-08-676-124-51	Sequence 51, Appl
286	33	41.8	325	2	US-09-949-016-7282	Sequence 7282, Ap	Sequence 7282, Ap	359	32	40.5	58	2	US-09-414-878-51	Sequence 51, Appl
287	33	41.8	325	2	US-09-949-016-7282	Sequence 7282, Ap	Sequence 7282, Ap	360	32	40.5	58	2	US-09-240-136-51	Sequence 51, Appl
288	33	41.8	333	2	US-09-248-796A-19280	Sequence 19280, A	Sequence 19280, A	361	32	40.5	58	2	US-09-638-770A-51	Sequence 51, Appl
289	33	41.8	339	2	US-09-489-039A-12070	Sequence 12070, A	Sequence 12070, A	362	32	40.5	58	2	US-10-167-351-51	Sequence 51, Appl
290	33	41.8	341	2	US-09-270-767-36808	Sequence 36808, A	Sequence 36808, A	363	32	40.5	64	2	US-09-270-767-58671	Sequence 58671, A
291	33	41.8	341	2	US-09-270-767-36808	Sequence 36808, A	Sequence 36808, A	364	32	40.5	66	2	US-09-248-796A-22637	Sequence 22637, A
292	33	41.8	362	2	US-09-594-669-6	Sequence 6, Appli	Sequence 6, Appli	365	32	40.5	66	2	US-09-513-993C-7449	Sequence 7449, Ap
293	33	41.8	362	2	US-10-112-432-6	Sequence 4, Appli	Sequence 4, Appli	366	32	40.5	77	2	US-09-248-796A-26998	Sequence 26998, A
294	33	41.8	391	2	US-09-594-669-4	Sequence 4, Appli	Sequence 4, Appli	367	32	40.5	82	2	US-09-936-697-10	Sequence 10, Appl
295	33	41.8	391	2	US-10-112-432-4	Sequence 12, Appl	Sequence 12, Appl	368	32	40.5	82	2	US-09-270-767-43328	Sequence 43328, A
296	33	41.8	405	2	US-09-594-669-12	Sequence 12, Appl	Sequence 12, Appl	369	32	40.5	90	2	US-09-134-001C-4887	Sequence 4887, Ap
297	33	41.8	405	2	US-10-112-432-12	Sequence 12, Appl	Sequence 12, Appl	370	32	40.5	93	2	US-09-543-681A-4385	Sequence 4385, Ap
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299	33	41.8	430	2	US-10-112-432-2	Sequence 2, Appli	Sequence 2, Appli	372	32	40.5	100	2	US-08-861-037-20	Sequence 20, Appl
300	33	41.8	434	2	US-09-594-669-10	Sequence 10, Appl	Sequence 10, Appl	373	32	40.5	111	2	PCT-US92-02044-4	Sequence 4, Appli
301	33	41.8	434	2	US-10-112-432-10	Sequence 10, Appl	Sequence 10, Appl	374	32	40.5	119	4	US-09-270-767-57534	Sequence 57534, A
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303	33	41.8	470	2	US-08-396-988-2	Sequence 2, Appli	Sequence 2, Appli	376	32	40.5	127	2	US-09-252-991A-18626	Sequence 18626, A
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305	33	41.8	470	2	US-09-391-104-26	Sequence 26, Appl	Sequence 26, Appl	378	32	40.5	142	2	US-09-902-540-12036	Sequence 12036, A
306	33	41.8	470	2	US-09-594-669-8	Sequence 8, Appli	Sequence 8, Appli	379	32	40.5	149	2	US-09-252-991A-24674	Sequence 24674, A
307	33	41.8	473	2	US-09-252-991A-25026	Sequence 25026, A	Sequence 25026, A	380	32	40.5	154	2	US-09-936-697-11	Sequence 11, Appl
308	33	41.8	473	2	US-10-112-432-8	Sequence 8, Appli	Sequence 8, Appli	381	32	40.5	173	2	US-09-270-767-41114	Sequence 41114, A
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310	33	41.8	478	2	US-09-252-991A-19298	Sequence 19298, A	Sequence 19298, A	383	32	40.5	173	2	US-09-270-767-53225	Sequence 53225, A
311	33	41.8	499	2	US-09-457-040B-13	Sequence 13, Appl	Sequence 13, Appl	384	32	40.5	180	2	US-09-252-991A-32026	Sequence 32026, A
312	33	41.8	499	2	US-09-905-999-21	Sequence 21, Appl	Sequence 21, Appl	385	32	40.5	183	2	US-09-270-767-37890	Sequence 37890, A
313	33	41.8	506	2	US-09-252-991A-27436	Sequence 27436, A	Sequence 27436, A	386	32	40.5	215	2	US-09-270-767-53107	Sequence 53107, A
314	33	41.8	601	2	US-09-489-039A-8499	Sequence 8499, Ap	Sequence 8499, Ap	387	32	40.5	191	2		
315	33	41.8	604	1	US-08-064-271-10	Sequence 10, Appl	Sequence 10, Appl	388	32	40.5	191	2		
316	33	41.8	604	1	US-08-487-753-4	Sequence 4, Appli	Sequence 4, Appli	389	32	40.5	191	2		
317	33	41.8	604	1	US-08-487-753-5	Sequence 5, Appli	Sequence 5, Appli	390	32	40.5	196	2		
318	33	41.8	604	1	US-08-480-065-5	Sequence 4, Appli	Sequence 4, Appli	391	32	40.5	215	2		
319	33	41.8	604	1	US-08-480-065-5	Sequence 5, Appli	Sequence 5, Appli	392	32	40.5	215	2		

393	32	40.5	217	2	US-09-107-532A-7168	Sequence 7168, Ap	466	32	40.5	688	2	US-09-949-016-11400	Sequence 11400, A
394	32	40.5	222	2	US-09-710-279-376	Sequence 376, App	467	32	40.5	715	2	US-09-543-681A-7603	Sequence 7603, Ap
395	32	40.5	223	2	US-09-134-001C-4829	Sequence 4829, Ap	468	32	40.5	720	2	US-09-583-110-2940	Sequence 2940, Ap
396	32	40.5	227	2	US-08-911-853-23	Sequence 23, Appl	469	32	40.5	720	2	US-09-107-433-4193	Sequence 4193, Ap
397	32	40.5	227	2	US-09-479-409-23	Sequence 23, Appl	470	32	40.5	746	2	US-09-949-016-10964	Sequence 10964, A
398	32	40.5	227	2	US-09-479-453-23	Sequence 23, Appl	471	32	40.5	819	2	US-09-489-039A-12105	Sequence 12105, A
399	32	40.5	243	2	US-09-640-211A-761	Sequence 761, App	472	32	40.5	830	2	US-09-064-199-19	Sequence 19, Appl
400	32	40.5	248	2	US-09-248-796A-19090	Sequence 19090, A	473	32	40.5	934	2	US-08-840-466A-19	Sequence 19, Appl
401	32	40.5	266	2	US-09-248-796A-19613	Sequence 19613, A	474	32	40.5	934	2	US-09-696-188B-19	Sequence 19, Appl
402	32	40.5	267	2	US-09-419-788-30	Sequence 30, Appl	475	32	40.5	934	2	US-10-150-058-19	Sequence 19, Appl
403	32	40.5	276	2	US-09-270-767-44401	Sequence 44401, A	476	32	40.5	934	2	US-08-837-459-19	Sequence 19, Appl
404	32	40.5	286	1	US-08-358-117-2	Sequence 11, Appl	477	32	40.5	935	2	US-09-914-259-25	Sequence 25, Appl
405	32	40.5	287	2	US-09-252-991A-30447	Sequence 30447, A	478	32	40.5	943	2	US-09-540-236-3458	Sequence 3458, Ap
406	32	40.5	309	2	US-09-107-532A-6518	Sequence 6518, Ap	479	32	40.5	950	2	Sequence 1, Appl	Sequence 1, Appl
407	32	40.5	318	2	US-09-270-767-42255	Sequence 42255, A	480	32	40.5	1014	2	US-09-134-000C-6265	Sequence 6265, Ap
408	32	40.5	326	2	US-08-866-381A-2	Sequence 2, Appl	481	32	40.5	1039	2	US-09-949-016-7859	Sequence 7859, Ap
409	32	40.5	326	2	US-09-280-598-52	Sequence 52, Appl	482	32	40.5	1060	2	US-09-248-796A-15476	Sequence 15476, A
410	32	40.5	326	2	US-09-489-039A-12537	Sequence 12537, A	483	32	40.5	1066	2	US-09-541-782-8	Sequence 8, Appl
411	32	40.5	344	2	US-09-147-236-11	Sequence 11, Appl	484	32	40.5	1066	2	US-09-723-820-8	Sequence 8, Appl
412	32	40.5	344	2	US-09-522-474-11	Sequence 11, Appl	485	32	40.5	1066	2	US-10-270-085-8	Sequence 8, Appl
413	32	40.5	348	2	US-09-252-991A-23520	Sequence 23520, A	486	32	40.5	1094	1	US-08-680-326-40	Sequence 40, Appl
414	32	40.5	349	2	US-09-540-236-3199	Sequence 3199, Ap	487	32	40.5	1106	2	US-09-064-199-17	Sequence 17, Appl
415	32	40.5	362	2	US-09-252-991A-16985	Sequence 16985, A	488	32	40.5	1111	2	US-09-914-259-28	Sequence 28, Appl
416	32	40.5	362	2	US-10-104-047-2732	Sequence 2732, Ap	489	32	40.5	1114	2	US-09-949-002-550	Sequence 550, App
417	32	40.5	376	2	US-09-270-767-32753	Sequence 32753, A	490	32	40.5	1130	1	US-08-519-547A-6	Sequence 6, Appl
418	32	40.5	376	2	US-09-270-767-47970	Sequence 47970, A	491	32	40.5	1130	2	US-09-064-199-18	Sequence 18, Appl
419	32	40.5	376	2	US-10-104-047-2623	Sequence 2623, Ap	492	32	40.5	1130	2	US-09-949-002-295	Sequence 295, App
420	32	40.5	387	2	US-10-000-489-112	Sequence 112, App	493	32	40.5	1137	2	US-09-902-481B-3	Sequence 3, Appl
421	32	40.5	410	2	US-09-347-801-10	Sequence 10, Appl	494	32	40.5	1137	2	US-09-902-481B-4	Sequence 4, Appl
422	32	40.5	410	2	US-09-854-731-10	Sequence 10, Appl	495	32	40.5	1137	2	US-09-902-481B-5	Sequence 5, Appl
423	32	40.5	412	2	US-09-252-991A-17935	Sequence 17935, A	496	32	40.5	1137	2	US-09-902-481B-6	Sequence 6, Appl
424	32	40.5	412	2	US-09-270-767-42908	Sequence 42908, A	497	32	40.5	1152	1	US-08-476-062A-43	Sequence 43, Appl
425	32	40.5	437	2	US-09-248-796A-16332	Sequence 16332, A	498	32	40.5	1152	4	US-08-476-062A-43	Sequence 43, Appl
426	32	40.5	437	2	US-09-489-039A-8154	Sequence 8154, Ap	499	32	40.5	1152	6	PCT-US96-01314-43	Patent No. 5424399
427	32	40.5	513	1	US-08-406-855A-21	Sequence 21, Appl	500	32	40.5	1153	1	US-08-173-497-3	Sequence 3, Appl
428	32	40.5	513	2	US-09-206-899-21	Sequence 21, Appl	501	32	40.5	1153	1	US-08-286-889-3	Sequence 3, Appl
429	32	40.5	513	2	US-09-724-519-6	Sequence 6, Appl	502	32	40.5	1153	1	US-08-485-618-3	Sequence 3, Appl
430	32	40.5	513	2	US-09-592-037-6	Sequence 6, Appl	503	32	40.5	1153	1	US-08-362-652-3	Sequence 3, Appl
431	32	40.5	513	2	US-09-428-156B-6	Sequence 6, Appl	504	32	40.5	1153	1	US-08-605-672-3	Sequence 3, Appl
432	32	40.5	513	2	US-09-949-016-10972	Sequence 10972, A	505	32	40.5	1153	1	US-08-482-293A-3	Sequence 3, Appl
433	32	40.5	514	2	US-09-902-540-10182	Sequence 10182, A	506	32	40.5	1153	1	US-08-943-363-3	Sequence 3, Appl
434	32	40.5	515	1	US-08-722-001-25	Sequence 25, Appl	507	32	40.5	1153	2	US-09-193-043-3	Sequence 3, Appl
435	32	40.5	515	2	US-09-032-742-5	Sequence 5, Appl	508	32	40.5	1153	2	US-09-688-307A-3	Sequence 3, Appl
436	32	40.5	515	2	US-09-688-415-9	Sequence 9, Appl	509	32	40.5	1153	2	US-09-350-259-3	Sequence 3, Appl
437	32	40.5	517	1	US-08-467-568-10	Sequence 10, Appl	510	32	40.5	1207	2	US-09-902-481B-1	Sequence 1, Appl
438	32	40.5	517	1	US-09-030-582-10	Sequence 10, Appl	511	32	40.5	1207	2	US-09-064-199-16	Sequence 16, Appl
439	32	40.5	520	1	US-08-334-698-4	Sequence 4, Appl	512	32	40.5	1882	2	US-09-369-364A-13	Sequence 13, Appl
440	32	40.5	520	1	US-08-228-932-4	Sequence 4, Appl	513	32	40.5	1882	2	US-08-938-105-3	Sequence 3, Appl
441	32	40.5	520	1	US-08-468-939-4	Sequence 4, Appl	514	32	40.5	1937	2	US-09-538-092-918	Sequence 918, App
442	32	40.5	520	1	US-08-406-855A-4	Sequence 4, Appl	515	32	40.5	1938	2	US-09-949-016-6417	Sequence 6417, Ap
443	32	40.5	520	1	US-08-722-190-4	Sequence 4, Appl	516	32	40.5	1939	2	US-09-310-187A-1	Sequence 1, Appl
444	32	40.5	520	2	US-08-244-354-4	Sequence 4, Appl	517	32	40.5	1939	2	US-09-538-092-915	Sequence 915, App
445	32	40.5	520	2	US-09-206-899-4	Sequence 4, Appl	518	32	40.5	1939	2	US-09-538-092-917	Sequence 917, App
446	32	40.5	520	2	US-09-444-783-4	Sequence 4, Appl	519	32	40.5	1939	2	US-09-949-016-6925	Sequence 6925, Ap
447	32	40.5	520	2	US-09-688-415-4	Sequence 4, Appl	520	32	40.5	1939	2	US-09-949-016-11104	Sequence 11104, A
448	32	40.5	520	2	US-09-444-783-4	Sequence 4, Appl	521	32	40.5	1940	2	US-09-538-092-901	Sequence 901, App
449	32	40.5	520	4	PCT-US95-04203-4	Sequence 4, Appl	522	32	40.5	1942	2	US-09-949-016-8135	Sequence 8135, Ap
450	32	40.5	532	2	US-09-487-558B-360	Sequence 360, App	523	32	40.5	1959	2	US-09-949-016-8134	Sequence 8888, Ap
451	32	40.5	534	2	US-09-124-541-1	Sequence 1, Appl	524	32	40.5	1963	2	US-09-949-016-8888	Sequence 2, Appl
452	32	40.5	534	2	US-09-663-326-1	Sequence 1, Appl	525	32	40.5	2289	2	US-09-051-019-2	Sequence 2, Appl
453	32	40.5	536	2	US-09-107-532A-5507	Sequence 5507, Ap	526	32	40.5	2556	1	US-08-185-432-17	Sequence 17, Appl
454	32	40.5	575	2	US-09-724-519-8	Sequence 8, Appl	527	32	40.5	2556	1	US-08-083-590A-20	Sequence 20, Appl
455	32	40.5	575	2	US-09-592-037-8	Sequence 8, Appl	528	32	40.5	2556	2	US-08-532-384-20	Sequence 2, Appl
456	32	40.5	575	2	US-09-428-156B-8	Sequence 8, Appl	529	32	40.5	2556	2	US-08-899-232-2	Sequence 2, Appl
457	32	40.5	610	2	US-09-252-991A-24942	Sequence 24942, A	530	32	40.5	2556	2	US-09-121-457-2	Sequence 2, Appl
458	32	40.5	618	2	US-08-866-381A-6	Sequence 6, Appl	531	32	40.5	2930	2	US-09-417-822-2	Sequence 2, Appl
459	32	40.5	621	1	US-08-208-887A-49	Sequence 49, Appl	532	32	40.5	2930	2	US-09-957-837A-2	Sequence 2, Appl
460	32	40.5	621	2	US-09-280-598-18	Sequence 18, Appl	533	31.5	39.9	52	2	US-09-959-897-50	Sequence 50, Appl
461	32	40.5	621	2	US-08-945-771-4	Sequence 4, Appl	534	31.5	39.9	338	2	US-09-634-957-4	Sequence 4, Appl
462	32	40.5	626	2	US-09-252-991A-20268	Sequence 20268, A	535	31.5	39.9	338	2	US-09-723-153-4	Sequence 4, Appl
463	32	40.5	637	1	US-10-100-252-4	Sequence 4, Appl	536	31.5	39.9	338	2	US-09-723-429-6	Sequence 6, Appl
464	32	40.5	673	1	US-08-455-073A-6	Sequence 6, Appl	537	31.5	39.9	392	2	US-09-796-487-6	Sequence 6, Appl
465	32	40.5	677	2	US-09-252-991A-32924	Sequence 32924, A	538	31.5	39.9	415	2	US-09-784-810C-15	Sequence 15, Appl

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541	31.5	39.9	790	2	US-09-634-957-2	Sequence 2, Appl1	614	31	39.2	312	2	US-10-104-047-2822	Sequence 2822, Ap
542	31.5	39.9	790	2	US-09-723-153-2	Sequence 2, Appl1	615	31	39.2	314	2	US-09-134-000C-5768	Sequence 5768, Ap
543	31.5	39.9	790	2	US-09-723-429-2	Sequence 2, Appl1	616	31	39.2	316	2	US-09-252-991A-21428	Sequence 21428, A
544	31.5	39.9	938	2	US-10-104-047-3855	Sequence 3855, Ap	617	31	39.2	317	2	US-09-540-236-3830	Sequence 3830, Ap
545	31	39.2	54	2	US-09-270-767-56761	Sequence 56761, A	618	31	39.2	319	2	US-09-724-510-2	Sequence 2, Appl1
546	31	39.2	60	2	US-09-248-796A-24618	Sequence 24618, A	619	31	39.2	319	2	US-09-723-216-2	Sequence 2, Appl1
547	31	39.2	71	2	US-09-143-470-20	Sequence 20, Appl1	620	31	39.2	319	2	US-09-675-227-2	Sequence 2, Appl1
548	31	39.2	71	2	US-09-107-532A-6543	Sequence 6543, Ap	621	31	39.2	336	2	US-09-252-991A-24121	Sequence 24121, A
549	31	39.2	73	2	US-09-328-352-8019	Sequence 8019, Ap	622	31	39.2	340	2	US-09-949-016-7280	Sequence 7280, Ap
550	31	39.2	75	2	US-09-621-976-6909	Sequence 6909, Ap	623	31	39.2	343	2	US-09-967-908A-8	Sequence 8, Appl1
551	31	39.2	89	2	US-09-248-796A-20387	Sequence 20387, A	624	31	39.2	343	2	US-10-159-151-8	Sequence 8, Appl1
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553	31	39.2	101	2	US-09-205-258-1124	Sequence 1124, Ap	626	31	39.2	362	2	US-09-252-991A-18494	Sequence 18494, A
554	31	39.2	101	2	US-09-621-976-4910	Sequence 4910, Ap	627	31	39.2	362	2	US-09-252-991A-31349	Sequence 31349, A
555	31	39.2	101	2	US-10-004-860-1124	Sequence 1124, Ap	628	31	39.2	363	2	US-09-967-908A-10	Sequence 10, Appl1
556	31	39.2	102	2	US-09-134-000C-5118	Sequence 5118, Ap	629	31	39.2	363	2	US-10-159-151-10	Sequence 10, Appl1
557	31	39.2	104	1	US-08-340-203A-7	Sequence 7, Appl1	630	31	39.2	364	2	US-09-270-767-34945	Sequence 34945, A
558	31	39.2	104	1	US-08-452-427-7	Sequence 7, Appl1	631	31	39.2	364	2	US-09-270-767-50162	Sequence 50162, A
559	31	39.2	104	2	US-09-085-407-7	Sequence 7, Appl1	632	31	39.2	373	2	US-09-967-908A-4	Sequence 4, Appl1
560	31	39.2	109	2	US-09-270-767-31915	Sequence 31915, A	633	31	39.2	373	2	US-10-159-151-4	Sequence 4, Appl1
561	31	39.2	110	2	US-09-640-211A-1012	Sequence 1012, Ap	634	31	39.2	376	2	US-09-328-352-8084	Sequence 8084, Ap
562	31	39.2	111	2	US-08-649-006A-2	Sequence 2, Appl1	635	31	39.2	380	2	US-09-638-937-11	Sequence 11, Appl1
563	31	39.2	111	2	US-09-771-023-2	Sequence 2, Appl1	636	31	39.2	380	2	US-09-248-796A-16419	Sequence 16419, A
564	31	39.2	115	2	US-09-248-796A-17476	Sequence 17476, A	637	31	39.2	381	2	US-09-967-908A-6	Sequence 6, Appl1
565	31	39.2	119	2	US-09-513-999C-6717	Sequence 6717, Ap	638	31	39.2	381	2	US-10-159-151-6	Sequence 6, Appl1
566	31	39.2	120	2	US-09-252-991A-19708	Sequence 19708, A	639	31	39.2	384	2	US-09-252-991A-27463	Sequence 27463, A
567	31	39.2	126	2	US-09-270-767-32337	Sequence 32337, A	640	31	39.2	384	2	US-09-270-767-46691	Sequence 46691, A
568	31	39.2	130	2	US-09-248-796A-14186	Sequence 14186, A	641	31	39.2	388	2	US-09-270-767-61007	Sequence 61007, A
569	31	39.2	131	1	US-08-466-583-6	Sequence 6, Appl1	642	31	39.2	389	2	US-09-725-945-2	Sequence 2, Appl1
570	31	39.2	131	2	US-08-265-427-6	Sequence 6, Appl1	643	31	39.2	394	2	US-08-791-115B-27	Sequence 27, Appl1
571	31	39.2	131	4	PCT-US95-07820-6	Sequence 6, Appl1	644	31	39.2	394	2	US-09-140-749-17	Sequence 17, Appl1
572	31	39.2	140	2	US-09-902-540-10461	Sequence 10461, A	645	31	39.2	397	2	US-08-991-426-4	Sequence 4, Appl1
573	31	39.2	145	1	US-08-470-179-32	Sequence 32, Appl1	646	31	39.2	397	2	US-09-143-470-4	Sequence 4, Appl1
574	31	39.2	159	2	US-09-640-211A-818	Sequence 818, Ap	647	31	39.2	397	2	US-08-649-006A-4	Sequence 4, Appl1
575	31	39.2	162	2	US-09-199-637A-431	Sequence 431, Ap	648	31	39.2	397	2	US-09-252-991A-26558	Sequence 26558, A
576	31	39.2	162	2	US-09-270-767-32851	Sequence 32851, A	649	31	39.2	397	2	US-09-771-023-4	Sequence 4, Appl1
577	31	39.2	162	2	US-09-270-767-42123	Sequence 42123, A	650	31	39.2	403	2	US-08-791-115B-1	Sequence 1, Appl1
578	31	39.2	162	2	US-09-270-767-48068	Sequence 48068, A	651	31	39.2	403	2	US-08-791-115B-23	Sequence 23, Appl1
579	31	39.2	171	2	US-09-605-703B-1696	Sequence 1696, Ap	652	31	39.2	403	2	US-08-791-115B-25	Sequence 25, Appl1
580	31	39.2	173	2	US-09-328-352-8078	Sequence 8078, Ap	653	31	39.2	403	2	US-09-140-749-2	Sequence 2, Appl1
581	31	39.2	189	2	US-09-216-393B-130	Sequence 130, Ap	654	31	39.2	403	2	US-09-140-749-10	Sequence 10, Appl1
582	31	39.2	189	2	US-09-538-092-553	Sequence 553, Ap	655	31	39.2	403	2	US-09-140-749-49	Sequence 49, Appl1
583	31	39.2	193	1	US-08-438-439C-21	Sequence 21, Appl1	656	31	39.2	403	2	US-09-140-749-55	Sequence 55, Appl1
584	31	39.2	193	2	US-09-270-767-57892	Sequence 57892, A	657	31	39.2	403	2	US-09-140-749-57	Sequence 57, Appl1
585	31	39.2	193	2	US-09-270-767-58950	Sequence 58950, A	658	31	39.2	403	2	US-09-870-379A-2	Sequence 2, Appl1
586	31	39.2	197	2	US-09-252-991A-21422	Sequence 21422, A	659	31	39.2	409	2	US-09-248-796A-18631	Sequence 18631, A
587	31	39.2	205	2	US-09-902-540-13272	Sequence 13272, A	660	31	39.2	409	2	US-09-902-540-10659	Sequence 10659, A
588	31	39.2	212	2	US-09-252-991A-23062	Sequence 23062, A	661	31	39.2	410	2	US-09-252-991A-22572	Sequence 22572, A
589	31	39.2	217	2	US-09-252-991A-24627	Sequence 24627, A	662	31	39.2	412	2	US-09-538-092-526	Sequence 526, App
590	31	39.2	224	2	US-09-252-991A-21765	Sequence 21765, A	663	31	39.2	414	2	US-09-248-796A-14798	Sequence 14798, A
591	31	39.2	231	2	US-09-270-767-61639	Sequence 61639, A	664	31	39.2	418	2	US-09-725-945-1	Sequence 1, Appl1
592	31	39.2	237	2	US-09-134-000C-6053	Sequence 6053, Ap	665	31	39.2	425	2	US-09-252-991A-32805	Sequence 32805, A
593	31	39.2	239	2	US-09-372-422A-42	Sequence 42, Appl1	666	31	39.2	427	2	US-09-902-540-15261	Sequence 15261, A
594	31	39.2	243	2	US-09-270-767-62302	Sequence 62302, A	667	31	39.2	430	2	US-08-791-115B-7	Sequence 7, Appl1
595	31	39.2	248	2	US-09-248-796A-27704	Sequence 27704, A	668	31	39.2	430	2	US-09-140-749-18	Sequence 18, Appl1
596	31	39.2	249	2	US-09-205-658-309	Sequence 309, Ap	669	31	39.2	439	2	US-09-248-796A-15968	Sequence 15968, A
597	31	39.2	250	2	US-09-248-796A-23347	Sequence 23347, A	670	31	39.2	445	2	US-10-104-047-2209	Sequence 2209, Ap
598	31	39.2	251	2	US-09-270-767-41536	Sequence 41536, A	671	31	39.2	455	2	US-09-252-991A-18265	Sequence 18265, A
599	31	39.2	256	2	US-08-956-171E-5228	Sequence 5228, Ap	672	31	39.2	462	1	US-08-267-092A-1	Sequence 1, Appl1
600	31	39.2	256	2	US-08-781-986A-5228	Sequence 5228, Ap	673	31	39.2	462	1	US-08-540-412-1	Sequence 1, Appl1
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602	31	39.2	266	2	US-09-252-991A-20635	Sequence 20635, A	675	31	39.2	462	2	US-08-468-161-1	Sequence 1, Appl1
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604	31	39.2	270	2	US-09-809-920-12	Sequence 12, Appl1	677	31	39.2	462	4	PCT-US95-08156-1	Sequence 1, Appl1
605	31	39.2	271	2	US-09-318-794A-2	Sequence 2, Appl1	678	31	39.2	464	2	US-08-970-134-3	Sequence 3, Appl1
606	31	39.2	271	2	US-09-318-794A-4	Sequence 4, Appl1	679	31	39.2	466	2	US-08-970-134-1	Sequence 1, Appl1
607	31	39.2	272	2	US-09-069-023-24	Sequence 24, Appl1	680	31	39.2	466	2	US-09-605-703B-2816	Sequence 2816, Ap
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687	31	39.2	523	2	US-09-949-016-11263	Sequence 1263, A	760	31	39.2	1180	2	US-09-459-715-8	Sequence 8, Appli
688	31	39.2	526	2	US-09-910-174B-9	Sequence 9, Appli	761	31	39.2	1212	1	US-08-072-574-10	Sequence 10, Appl
689	31	39.2	526	2	US-09-620-461-9	Sequence 9, Appli	762	31	39.2	1212	1	US-08-486-270-10	Sequence 10, Appl
690	31	39.2	526	2	US-09-949-016-6122	Sequence 6122, Ap	763	31	39.2	1212	2	US-08-367-264-10	Sequence 10, Appl
691	31	39.2	533	2	US-09-360-197-10	Sequence 10, Appl	764	31	39.2	1212	2	US-08-660-148-5	Sequence 5, Appli
692	31	39.2	534	2	US-09-949-016-8945	Sequence 8945, Ap	765	31	39.2	1212	2	US-09-153-757-10	Sequence 10, Appl
693	31	39.2	534	2	US-09-613-486-44	Sequence 44, Appl	766	31	39.2	1212	2	US-09-459-715-10	Sequence 10, Appl
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697	31	39.2	559	2	US-09-140-749-15	Sequence 15, Appl	770	31	39.2	1368	2	US-10-159-151-2	Sequence 2, Appli
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699	31	39.2	565	2	US-08-908-156A-12	Sequence 12, Appl	772	31	39.2	1839	2	US-09-404-108-4	Sequence 4, Appli
700	31	39.2	571	1	US-07-955-905A-25	Sequence 25, Appl	773	31	39.2	2753	2	US-09-949-016-7659	Sequence 7659, Ap
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702	31	39.2	579	2	US-09-252-991A-28652	Sequence 28652, A	775	31	39.2	2753	2	US-09-949-016-7660	Sequence 7660, Ap
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705	31	39.2	597	2	US-09-140-749-8	Sequence 8, Appli	778	30.5	38.6	256	2	US-09-538-092-1246	Sequence 1246, Ap
706	31	39.2	598	2	US-09-270-767-45086	Sequence 45086, A	779	30.5	38.6	299	2	US-09-328-352-5216	Sequence 5216, Ap
707	31	39.2	600	2	US-09-543-681A-4196	Sequence 4196, Ap	780	30.5	38.6	299	2	US-09-991-181-213	Sequence 213, App
708	31	39.2	607	2	US-09-949-016-6293	Sequence 6293, Ap	781	30.5	38.6	299	2	US-09-991-181-213	Sequence 213, App
709	31	39.2	616	2	US-09-248-796A-14992	Sequence 14992, A	782	30.5	38.6	299	2	US-09-997-333-213	Sequence 213, App
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711	31	39.2	645	2	US-09-328-501-1	Sequence 1, Appli	784	30.5	38.6	332	2	US-09-997-333-213	Sequence 213, App
712	31	39.2	645	2	US-08-791-115B-6	Sequence 6, Appli	785	30.5	38.6	332	2	US-09-997-333-213	Sequence 213, App
713	31	39.2	646	2	US-09-777-710A-1	Sequence 1, Appli	786	30.5	38.6	332	2	US-09-997-333-213	Sequence 213, App
714	31	39.2	646	5	US-10-191-289A-1	Sequence 1, Appli	787	30.5	38.6	332	2	US-09-997-333-213	Sequence 213, App
715	31	39.2	646	2	US-09-489-039A-12514	Sequence 12514, A	788	30.5	38.6	332	2	US-09-997-333-213	Sequence 213, App
716	31	39.2	659	2	US-09-710-279-1596	Sequence 1596, Ap	789	30.5	38.6	332	2	US-09-997-333-213	Sequence 213, App
717	31	39.2	666	2	US-09-489-039A-12388	Sequence 12388, A	790	30.5	38.6	332	2	US-09-997-333-213	Sequence 213, App
718	31	39.2	670	2	US-09-328-501-15	Sequence 15, Appl	791	30.5	38.6	332	2	US-09-997-333-213	Sequence 213, App
719	31	39.2	670	2	US-09-777-710A-15	Sequence 15, Appl	792	30.5	38.6	332	2	US-09-997-333-213	Sequence 213, App
720	31	39.2	670	5	US-10-191-289A-15	Sequence 15, Appl	793	30.5	38.6	332	2	US-09-997-333-213	Sequence 213, App
721	31	39.2	686	2	US-09-252-991A-29396	Sequence 29396, A	794	30.5	38.6	332	2	US-09-997-333-213	Sequence 213, App
722	31	39.2	690	2	US-09-134-001C-4938	Sequence 4938, Ap	795	30.5	38.6	332	2	US-09-997-333-213	Sequence 213, App
723	31	39.2	704	2	US-09-949-002-407	Sequence 407, App	796	30.5	38.6	332	2	US-09-997-333-213	Sequence 213, App
724	31	39.2	705	2	US-09-949-016-11418	Sequence 11418, A	797	30.5	38.6	332	2	US-09-997-333-213	Sequence 213, App
725	31	39.2	705	2	US-09-949-002-557	Sequence 557, App	798	30.5	38.6	332	2	US-09-997-333-213	Sequence 213, App
726	31	39.2	726	2	US-09-252-991A-17064	Sequence 17064, A	799	30.5	38.6	332	2	US-09-997-333-213	Sequence 213, App
727	31	39.2	730	2	US-09-291-170A-3	Sequence 3, Appli	800	30.5	38.6	332	2	US-09-997-333-213	Sequence 213, App
728	31	39.2	730	2	US-09-724-884-3	Sequence 3, Appli	801	30.5	38.6	332	2	US-09-997-333-213	Sequence 213, App
729	31	39.2	730	2	US-09-724-592-3	Sequence 3, Appli	802	30.5	38.6	332	2	US-09-997-333-213	Sequence 213, App
730	31	39.2	730	2	US-09-673-222-3	Sequence 3, Appli	803	30.5	38.6	332	2	US-09-997-333-213	Sequence 213, App
731	31	39.2	742	2	US-08-791-115B-5	Sequence 5, Appli	804	30.5	38.6	332	2	US-09-997-333-213	Sequence 213, App
732	31	39.2	762	2	US-09-270-767-42580	Sequence 42580, A	805	30.5	38.6	332	2	US-09-997-333-213	Sequence 213, App
733	31	39.2	777	2	US-09-270-767-45498	Sequence 45498, A	806	30.5	38.6	332	2	US-09-997-333-213	Sequence 213, App
734	31	39.2	818	2	US-09-328-352-5208	Sequence 5208, Ap	807	30.5	38.6	332	2	US-09-997-333-213	Sequence 213, App
735	31	39.2	822	2	US-09-270-767-43578	Sequence 43578, A	808	30.5	38.6	332	2	US-09-997-333-213	Sequence 213, App
736	31	39.2	824	2	US-09-270-767-45676	Sequence 45676, A	809	30.5	38.6	332	2	US-09-997-333-213	Sequence 213, App
737	31	39.2	843	1	US-09-172-977-3	Sequence 3, Appli	810	30.5	38.6	332	2	US-09-997-333-213	Sequence 213, App
738	31	39.2	843	2	US-09-404-108-3	Sequence 3, Appli	811	30.5	38.6	332	2	US-09-997-333-213	Sequence 213, App
739	31	39.2	877	1	US-08-072-574-12	Sequence 12, Appl	812	30.5	38.6	332	2	US-09-997-333-213	Sequence 213, App
740	31	39.2	877	1	US-08-486-270-12	Sequence 12, Appl	813	30.5	38.6	332	2	US-09-997-333-213	Sequence 213, App
741	31	39.2	877	2	US-08-367-264-12	Sequence 12, Appl	814	30.5	38.6	332	2	US-09-997-333-213	Sequence 213, App
742	31	39.2	877	2	US-09-153-757-12	Sequence 12, Appl	815	30.5	38.6	332	2	US-09-997-333-213	Sequence 213, App
743	31	39.2	877	2	US-09-459-715-12	Sequence 12, Appl	816	30.5	38.6	332	2	US-09-997-333-213	Sequence 213, App
744	31	39.2	904	2	US-09-248-796A-15547	Sequence 15547, A	817	30.5	38.6	332	2	US-09-997-333-213	Sequence 213, App
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747	31	39.2	975	2	US-09-695-481-4	Sequence 2, Appli	820	30.5	38.6	332	2	US-09-997-333-213	Sequence 213, App
748	31	39.2	1027	1	US-08-551-437-2	Sequence 2, Appli	821	30.5	38.6	332	2	US-09-997-333-213	Sequence 213, App
749	31	39.2	1027	2	US-09-004-225-2	Sequence 2, Appli	822	30.5	38.6	332	2	US-09-997-333-213	Sequence 213, App
750	31	39.2	1027	2	US-09-084-346-2	Sequence 2, Appli	823	30.5	38.6	332	2	US-09-997-333-213	Sequence 213, App
751	31	39.2	1027	2	US-09-104-704-2	Sequence 2, Appli	824	30.5	38.6	332	2	US-09-997-333-213	Sequence 213, App
752	31	39.2	1164	2	US-09-457-708-2	Sequence 2, Appli	825	30.5	38.6	332	2	US-09-997-333-213	Sequence 213, App
753	31	39.2	1164	2	US-09-950-046A-2	Sequence 2, Appli	826	30.5	38.6	332	2	US-09-997-333-213	Sequence 213, App
754	31	39.2	1164	2	US-09-976-594-989	Sequence 989, App	827	30.5	38.6	332	2	US-09-997-333-213	Sequence 213, App
755	31	39.2	1180	1	US-08-072-574-8	Sequence 8, Appli	828	30.5	38.6	332	2	US-09-997-333-213	Sequence 213, App
756	31	39.2	1180	1	US-08-486-270-8	Sequence 8, Appli	829	30.5	38.6	332	2	US-09-997-333-213	Sequence 213, App
757	31	39.2	1180	2	US-08-367-264-8	Sequence 8, Appli	830	30.5	38.6	332	2	US-09-997-333-213	Sequence 213, App

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834	30	38.0	157	1	US-08-208-887A-8	Sequence 8, Appli	907	30	38.0	276	2	US-09-510-322A-11	Sequence 11, Appli
835	30	38.0	157	1	US-08-538-005-8	Sequence 8, Appli	908	30	38.0	276	2	US-09-236-268-6	Sequence 6, Appli
836	30	38.0	157	2	US-09-280-598-9	Sequence 9, Appli	909	30	38.0	277	2	US-09-514-768B-11	Sequence 11, Appli
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839	30	38.0	160	1	US-08-208-887A-40	Sequence 40, Appli	912	30	38.0	281	2	US-08-232-931A-29199	Sequence 29199, A
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841	30	38.0	160	2	US-09-280-598-37	Sequence 37, Appli	914	30	38.0	283	2	US-09-248-796A-14507	Sequence 14507, A
842	30	38.0	167	2	US-09-439-313-481	Sequence 481, App	915	30	38.0	286	2	US-09-198-452A-277	Sequence 277, App
843	30	38.0	167	2	US-09-636-215-481	Sequence 481, App	916	30	38.0	296	2	US-09-248-796A-14696	Sequence 14696, A
844	30	38.0	167	2	US-09-685-166A-481	Sequence 481, App	917	30	38.0	297	2	US-09-583-110-3131	Sequence 3131, Ap
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846	30	38.0	167	2	US-09-270-767-53685	Sequence 53685, A	919	30	38.0	299	2	US-09-724-508-2	Sequence 2, Appli
847	30	38.0	167	2	US-09-679-426-481	Sequence 481, App	920	30	38.0	299	2	US-09-724-508-2	Sequence 2, Appli
848	30	38.0	167	2	US-09-759-143-481	Sequence 481, App	921	30	38.0	299	2	US-10-090-695-2	Sequence 2, Appli
849	30	38.0	167	2	US-09-651-236-481	Sequence 481, App	922	30	38.0	301	2	US-09-438-185A-267	Sequence 267, App
850	30	38.0	167	2	US-09-657-279-481	Sequence 481, App	923	30	38.0	304	2	US-09-107-532A-5051	Sequence 5051, Ap
851	30	38.0	167	2	US-10-012-896-481	Sequence 481, App	924	30	38.0	304	2	US-09-636-215-835	Sequence 835, App
852	30	38.0	168	2	US-09-270-767-41447	Sequence 41447, A	925	30	38.0	304	2	US-09-685-166A-835	Sequence 835, App
853	30	38.0	169	2	US-09-248-796A-14549	Sequence 14549, A	926	30	38.0	304	2	US-09-679-426-835	Sequence 835, App
854	30	38.0	170	2	US-09-270-767-46064	Sequence 46064, A	927	30	38.0	304	2	US-09-759-143-835	Sequence 835, App
855	30	38.0	173	2	US-09-071-035-332	Sequence 332, App	928	30	38.0	304	2	US-09-651-236-835	Sequence 835, App
856	30	38.0	173	2	US-10-206-576-332	Sequence 332, App	929	30	38.0	304	2	US-09-902-540-10990	Sequence 10990, A
857	30	38.0	174	2	US-09-198-452A-334	Sequence 334, App	930	30	38.0	304	2	US-09-657-279-835	Sequence 835, App
858	30	38.0	174	2	US-09-486-147-41	Sequence 41, Appli	931	30	38.0	304	2	US-10-012-896-835	Sequence 835, App
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861	30	38.0	176	2	US-09-949-016-9191	Sequence 9191, Ap	934	30	38.0	310	2	US-09-248-796A-17322	Sequence 17322, A
862	30	38.0	197	2	US-09-107-433-4379	Sequence 4379, Ap	935	30	38.0	312	2	US-09-328-352-8015	Sequence 8015, Ap
863	30	38.0	206	2	US-09-248-796A-14304	Sequence 14304, A	936	30	38.0	317	2	US-09-583-110-3082	Sequence 3082, Ap
864	30	38.0	212	2	US-09-270-767-44150	Sequence 44150, A	937	30	38.0	317	2	US-09-769-787-65	Sequence 65, Appli
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868	30	38.0	227	2	US-09-252-991A-27681	Sequence 27681, A	941	30	38.0	322	2	US-09-879-957-198	Sequence 198, App
869	30	38.0	229	2	US-08-751-359-22	Sequence 22, Appli	942	30	38.0	326	2	US-09-270-767-36864	Sequence 36864, A
870	30	38.0	229	2	US-08-907-146-22	Sequence 22, Appli	943	30	38.0	326	2	US-09-270-767-52081	Sequence 52081, A
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873	30	38.0	235	2	US-09-107-433-43222	Sequence 43222, Ap	946	30	38.0	335	2	US-09-902-540-11829	Sequence 11829, A
874	30	38.0	240	2	US-09-270-767-43222	Sequence 43222, Ap	947	30	38.0	346	1	US-07-895-300A-1	Sequence 1, Appli
875	30	38.0	246	2	US-09-252-991A-16586	Sequence 16586, A	948	30	38.0	346	1	US-08-458-367-1	Sequence 1, Appli
876	30	38.0	250	2	US-09-710-279-2310	Sequence 2310, Ap	949	30	38.0	346	2	US-09-638-112-1	Sequence 1, Appli
877	30	38.0	252	2	US-09-248-796A-26644	Sequence 26644, A	950	30	38.0	346	2	US-10-155-407A-1	Sequence 1, Appli
878	30	38.0	255	2	US-09-248-796A-18600	Sequence 18600, A	951	30	38.0	346	4	PCT-US93-05136-1	Sequence 1, Appli
879	30	38.0	260	2	US-09-796-774-1	Sequence 1, Appli	952	30	38.0	350	1	US-08-415-751-15	Sequence 15, Appli
880	30	38.0	260	2	US-08-663-831-1	Sequence 1, Appli	953	30	38.0	350	2	US-08-909-828-1	Sequence 1, Appli
881	30	38.0	260	2	US-08-663-831-7	Sequence 7, Appli	954	30	38.0	350	2	US-08-909-828-2	Sequence 2, Appli
882	30	38.0	260	2	US-08-663-831-8	Sequence 8, Appli	955	30	38.0	350	2	US-09-543-681A-4580	Sequence 4580, Ap
883	30	38.0	260	2	US-08-663-831-9	Sequence 9, Appli	956	30	38.0	350	2	US-09-538-092-97	Sequence 97, Appli
884	30	38.0	260	2	US-08-663-831-10	Sequence 10, Appli	957	30	38.0	350	2	US-09-725-957-1	Sequence 1, Appli
885	30	38.0	260	2	US-08-663-831-11	Sequence 11, Appli	958	30	38.0	350	2	US-09-725-957-2	Sequence 2, Appli
886	30	38.0	260	2	US-08-663-831-12	Sequence 12, Appli	959	30	38.0	354	2	US-09-198-452A-852	Sequence 852, App
887	30	38.0	260	2	US-08-663-831-13	Sequence 13, Appli	960	30	38.0	354	2	US-09-438-185A-801	Sequence 801, App
888	30	38.0	260	2	US-10-074-509-4	Sequence 4, Appli	961	30	38.0	355	2	US-09-724-511-4	Sequence 4, Appli
889	30	38.0	260	2	US-09-489-039A-11187	Sequence 11187, A	962	30	38.0	355	2	US-09-723-097-4	Sequence 4, Appli
890	30	38.0	260	2	US-10-360-101-224	Sequence 224, App	963	30	38.0	355	2	US-09-632-344-4	Sequence 4, Appli
891	30	38.0	261	2	US-09-252-991A-19759	Sequence 19759, A	964	30	38.0	356	2	US-09-270-767-44479	Sequence 44479, A
892	30	38.0	262	2	US-09-543-681A-8282	Sequence 8282, Ap	965	30	38.0	357	2	US-09-328-352-4987	Sequence 4987, Ap
893	30	38.0	263	2	US-09-328-352-5801	Sequence 5801, Ap	966	30	38.0	357	2	US-09-489-039A-10510	Sequence 10510, A
894	30	38.0	264	2	US-09-198-452A-486	Sequence 486, App	967	30	38.0	365	2	US-10-104-047-3375	Sequence 3375, Ap
895	30	38.0	266	2	US-09-439-313-534	Sequence 534, App	968	30	38.0	367	2	US-09-724-511-2	Sequence 2, Appli
896	30	38.0	266	2	US-09-636-215-534	Sequence 534, App	969	30	38.0	367	2	US-09-723-097-2	Sequence 2, Appli
897	30	38.0	266	2	US-09-685-166A-534	Sequence 534, App	970	30	38.0	367	2	US-09-632-344-2	Sequence 2, Appli
898	30	38.0	266	2	US-09-679-426-534	Sequence 534, App	971	30	38.0	370	2	US-09-328-352-5285	Sequence 5285, Ap
899	30	38.0	266	2	US-09-759-143-534	Sequence 534, App	972	30	38.0	374	2	US-09-107-532A-6027	Sequence 6027, Ap
900	30	38.0	266	2	US-09-651-236-534	Sequence 534, App	973	30	38.0	375	2	US-09-252-991A-24216	Sequence 24216, A
901	30	38.0	266	2	US-09-657-279-534	Sequence 534, App	974	30	38.0	375	2	US-09-538-092-1082	Sequence 1082, Ap
902	30	38.0	266	2	US-10-012-896-534	Sequence 534, App	975	30	38.0	375	2	US-09-949-016-6369	Sequence 6369, Ap
903	30	38.0	269	2	US-09-489-039A-13046	Sequence 13046, A	976	30	38.0	377	2	US-09-538-092-939	Sequence 939, App

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977 30 38.0 377 2 US-09-949-016-6693 Sequence 6693, Ap
978 30 38.0 381 2 US-09-949-016-9555 Sequence 9555, Ap
979 30 38.0 382 2 US-09-270-767-34944 Sequence 34944, A
980 30 38.0 382 2 US-09-270-767-50161 Sequence 50161, A
981 30 38.0 385 2 US-10-644-123A-9 Sequence 9, Appl
982 30 38.0 386 2 US-09-949-016-10070 Sequence 10070, A
983 30 38.0 394 2 US-09-252-991A-22328 Sequence 22328, A
984 30 38.0 398 2 US-09-107-532A-4688 Sequence 4688, A
985 30 38.0 398 2 US-09-583-110-2908 Sequence 2908, Ap
986 30 38.0 401 2 US-09-005-298-17 Sequence 17, Appl
987 30 38.0 401 2 US-08-768-619-17 Sequence 17, Appl
988 30 38.0 401 4 PCT-US96-09848-31 Sequence 31, Appl
989 30 38.0 402 2 US-09-270-767-41627 Sequence 41627, A
990 30 38.0 404 2 US-09-153-599A-8 Sequence 8, Appl
991 30 38.0 406 2 US-09-107-433-4017 Sequence 4017, Ap
992 30 38.0 407 2 US-09-005-298-15 Sequence 15, Appl
993 30 38.0 407 2 US-08-768-619-15 Sequence 15, Appl
994 30 38.0 407 4 PCT-US96-09848-15 Sequence 15, Appl
995 30 38.0 409 1 US-08-924-254-2 Sequence 2, Appl
996 30 38.0 409 2 US-09-120-249-2 Sequence 2, Appl
997 30 38.0 411 2 US-09-347-801-22 Sequence 22, Appl
998 30 38.0 411 2 US-09-854-731-22 Sequence 22, Appl
999 30 38.0 412 2 US-09-252-991A-18512 Sequence 18512, A
1000 30 38.0 425 2 US-09-538-092-879 Sequence 879, App
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ALIGNMENTS

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RESULT 1
US-09-595-684B-31
; Sequence 31, Application US/09595684B
; Patent No. 654766
; GENERAL INFORMATION:
; APPLICANT: Beraud, Christophe
; APPLICANT: Ohashi, Cara
; APPLICANT: Sakowicz, Roman
; APPLICANT: Vaisberg, Eugeni
; APPLICANT: Wood, Kenneth
; APPLICANT: Yu, Ming
; TITLE OF INVENTION: Human kinesins and methods of producing
; TITLE OF INVENTION: and purifying human kinesins
; FILE REFERENCE: cytop036
; CURRENT APPLICATION NUMBER: US/09/595,684B
; CURRENT FILING DATE: 2002-06-24
; PRIOR APPLICATION NUMBER: 09/295,612
; PRIOR FILING DATE: 2000-04-20
; NUMBER OF SEQ ID NOS: 105
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 31
; LENGTH: 2662
; TYPE: PRT
; ORGANISM: Human
US-09-595-684B-31

Query Match 100.0%; Score 79; DB 2; Length 2662;
Best Local Similarity 100.0%; Pred. No. 2.1e-05;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RHYGETKMNQRSSRS 15
Db 189 RHYGETKMNQRSSRS 203

RESULT 2
US-09-538-092-1252
; Sequence 1252, Application US/09538092
; Patent No. 6753314
; GENERAL INFORMATION:
; APPLICANT: Giot, Loic
; APPLICANT: Mansfield, Traci A.
; TITLE OF INVENTION: Protein-Protein Complexes and Method of Using Same
; FILE REFERENCE: 15966-542
; CURRENT APPLICATION NUMBER: US/09/538,092
; CURRENT FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: 60/127,352
; PRIOR FILING DATE: 1999-04-01
; PRIOR APPLICATION NUMBER: 60/178,965
; PRIOR FILING DATE: 2000-02-01
; NUMBER OF SEQ ID NOS: 1387
; SOFTWARE: CurPatSeqFormatter Version 0.9
; SEQ ID NO 1252
; LENGTH: 2663
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (0)..(0)
; OTHER INFORMATION: Polypeptide Accession Number Q02224
US-09-538-092-1252

Query Match 100.0%; Score 79; DB 2; Length 2663;
Best Local Similarity 100.0%; Pred. No. 2.1e-05;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RHYGETKMNQRSSRS 15
Db 189 RHYGETKMNQRSSRS 203

RESULT 3
US-09-150-867-1
; Sequence 1, Application US/09150867
; Patent No. 6645748
; GENERAL INFORMATION:
; APPLICANT: Wood, Kenneth W.
; APPLICANT: Sakowicz, Roman
; APPLICANT: Goldstein, Lawrence S.B.
; APPLICANT: Cleveland, Don W.
; APPLICANT: The Regents of the University of California
; TITLE OF INVENTION: Plus End-Directed Microtubule Motor Required for
; FILE REFERENCE: 18557C-000110US
; CURRENT APPLICATION NUMBER: US/09/150,867
; CURRENT FILING DATE: 1998-09-10
; EARLIER APPLICATION NUMBER: US 60/058,645
; EARLIER FILING DATE: 1997-09-11
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 2954
; TYPE: PRT
; ORGANISM: Xenopus sp.
; FEATURE:
; OTHER INFORMATION: Xenopus centromere-associated protein-E (XCENP-E)
; OTHER INFORMATION: member of the kinesin superfamily of microtubule
; OTHER INFORMATION: motor proteins
; FEATURE:
; NAME/KEY: DOMAIN
; LOCATION: (1)..(472)
; OTHER INFORMATION: kinesin like motor domain
; FEATURE:
; NAME/KEY: DOMAIN
; LOCATION: (473)..(2752)
; OTHER INFORMATION: rod domain
; FEATURE:
; NAME/KEY: DOMAIN
; LOCATION: (2753)..(2954)
; OTHER INFORMATION: tail domain
US-09-150-867-1

Query Match 87.3%; Score 69; DB 2; Length 2954;
Best Local Similarity 86.7%; Pred. No. 0.0015;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 RHYGETKMNQRSSRS 15
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Db      187 RHYGETKNDHSSRS 201
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RESULT 4
US-08-006-676B-1
; Sequence 1, Application US/08006676B
; Patent No. 5411865
; GENERAL INFORMATION:
; APPLICANT: Reed, Steven
; TITLE OF INVENTION: Diagnosis of Leishmaniasis
; NUMBER OF SEQUENCES: 3
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Jeffrey B. Oster
; STREET: 8339 SE 57th Street
; CITY: Mercer Island
; STATE: Washington
; COUNTRY: USA
; ZIP: 98040-4906
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WORD for Windows
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/006,676B
; FILING DATE: 15-JAN-1993
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Oster, Jeffrey B.
; REGISTRATION NUMBER: 32,585
; REFERENCE/DOCKET NUMBER: REED-4
; TELEPHONE: (206) 232 7845
; TELEFAX: (206) 236 0205
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 955 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-006-676B-1

Query Match      68.4%; Score 54; DB 1; Length 955;
Best Local Similarity 73.3%; Pred. No. 0.24;
Matches 11; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY      1 RHYGETKNDHSSRS 15
|||
Db      241 RHTASTKNDHSSRS 255
|||||

RESULT 5
US-08-282-845-2
; Sequence 2, Application US/08282845
; Patent No. 5719263
; GENERAL INFORMATION:
; APPLICANT: Reed, Steven G.
; TITLE OF INVENTION: A 230kd Antigen Present in Leishmania
; NUMBER OF SEQUENCES: 3
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Immunex Corporation
; STREET: 51 University Street
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Apple Macintosh Operating System 7.1
; SOFTWARE: Microsoft Word for Macintosh 5.1a

Query Match      68.4%; Score 54; DB 1; Length 955;
Best Local Similarity 73.3%; Pred. No. 0.24;
Matches 11; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY      1 RHYGETKNDHSSRS 15
|||
Db      241 RHTASTKNDHSSRS 255
|||||

RESULT 6
US-08-428-414A-3
; Sequence 3, Application US/08428414A
; Patent No. 5912166
; GENERAL INFORMATION:
; APPLICANT: Reed, Steven G.
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR DIAGNOSIS OF
; TITLE OF INVENTION: LEISHMANIASIS
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SEED and BERRY
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: USA
; ZIP: 98104-7092
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/428,414A
; FILING DATE: 21-APR-1995
; CLASSIFICATION: 436
; ATTORNEY/AGENT INFORMATION:
; NAME: Kadlecak, Ann T.
; REGISTRATION NUMBER: 39,244
; REFERENCE/DOCKET NUMBER: 210121.407
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; TELEEX: 3723836 SEEDANDBERRY
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 955 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
US-08-428-414A-3
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Query Match      68.4%; Score 54; DB 1; Length 955;
Best Local Similarity 73.3%; Pred. No. 0.24;
Matches 11; Conservative 0; Mismatches 4; Indels 4; Gaps 0;

Qy      1 RHYGETKNQRRSSRS 15
Db      241 RHTASTKMDRRSSRS 255

RESULT 7
PCT-US94-00324-1
; Sequence 1, Application PC/TUS9400324
; GENERAL INFORMATION:
; APPLICANT: Reed, Steven
; TITLE OF INVENTION: Diagnosis of Leishmaniasis
; NUMBER OF SEQUENCES: 3
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Immunex Corporation
; STREET: 51 University Street
; CITY: Seattle
; STATE: Washington
; COUNTRY: USA
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Apple System 7.1
; SOFTWARE: Microsoft Word, version 5.1a
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US94/00324
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/006,676
; FILING DATE: 15-JAN-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Perkins, Patricia Anne
; REGISTRATION NUMBER: 34,693
; REFERENCE/DOCKET NUMBER: 5004-WO
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 587-0430
; TELEFAX: (206) 233-0644
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 955 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
PCT-US94-00324-1

Query Match      68.4%; Score 54; DB 4; Length 955;
Best Local Similarity 73.3%; Pred. No. 0.24;
Matches 11; Conservative 0; Mismatches 4; Indels 4; Gaps 0;

Qy      1 RHYGETKNQRRSSRS 15
Db      241 RHTASTKMDRRSSRS 255

RESULT 8
US-09-724-517-4
; Sequence 4, Application US/09724517
; Patent No. 6379941
; GENERAL INFORMATION:
; APPLICANT: Beraud, Christophe
; APPLICANT: Freedman, Richard
; TITLE OF INVENTION: No. 6379941el motor proteins and methods for
; TITLE OF INVENTION: their use
; FILE REFERENCE: 1031
; CURRENT APPLICATION NUMBER: US/09/724,517
; CURRENT FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: US/09/641,807
; PRIOR FILING DATE: 2000-08-17

Query Match      65.8%; Score 52; DB 2; Length 341;
Best Local Similarity 66.7%; Pred. No. 0.19;
Matches 10; Conservative 2; Mismatches 3; Indels 3; Gaps 0;

Qy      1 RHYGETKNQRRSSRS 15
Db      192 RHTGTQMKNEHSRS 206

RESULT 9
US-09-641-807A-4
; Sequence 4, Application US/09641807A
; Patent No. 6440731
; GENERAL INFORMATION:
; APPLICANT: Beraud, Christophe
; APPLICANT: Freedman, Richard
; TITLE OF INVENTION: No. 6440731el motor proteins and methods for
; TITLE OF INVENTION: their use
; FILE REFERENCE: 1031
; CURRENT APPLICATION NUMBER: US/09/641,807A
; CURRENT FILING DATE: 2000-08-17
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 341
; TYPE: PRT
; ORGANISM: Human
US-09-641-807A-4

Query Match      65.8%; Score 52; DB 2; Length 341;
Best Local Similarity 66.7%; Pred. No. 0.19;
Matches 10; Conservative 2; Mismatches 3; Indels 3; Gaps 0;

Qy      1 RHYGETKNQRRSSRS 15
Db      192 RHTGTQMKNEHSRS 206

RESULT 10
US-09-723-096-4
; Sequence 4, Application US/09723096
; Patent No. 6448026
; GENERAL INFORMATION:
; APPLICANT: Beraud, Christophe
; APPLICANT: Freedman, Richard
; TITLE OF INVENTION: No. 6448026el motor proteins and methods for
; TITLE OF INVENTION: their use
; FILE REFERENCE: 1031
; CURRENT APPLICATION NUMBER: US/09/723,096
; CURRENT FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: US/09/641,807
; PRIOR FILING DATE: 2000-08-17
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 341
; TYPE: PRT
; ORGANISM: Human
US-09-723-096-4

Query Match      65.8%; Score 52; DB 2; Length 341;
Best Local Similarity 66.7%; Pred. No. 0.19;
Matches 10; Conservative 2; Mismatches 3; Indels 3; Gaps 0;

Qy      1 RHYGETKNQRRSSRS 15
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; CURRENT APPLICATION NUMBER: US/10/093,317
; CURRENT FILING DATE: 2002-03-06
; PRIOR APPLICATION NUMBER: 09/724,224
; PRIOR FILING DATE: 2000-11-28
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 346
; TYPE: PRT
; ORGANISM: Human
US-10-093-317-6

Query Match      62.0%; Score 49; DB 2; Length 346;
Best Local Similarity 66.7%; Pred. No. 0.66;
Matches 10; Conservative 2; Mismatches 3; Indels 3; Gaps 0;

Qy      1 RHYGETKNQSRSS 15
      | | | | | | | |
Db      208 RTVGATRLNQSRSS 222
      | | | | | | | |

RESULT 15
US-09-724-224-2
; Sequence 2, Application US/09724224
; Patent No. 6387644
; GENERAL INFORMATION:
; APPLICANT: Beraud, Christophe
; TITLE OF INVENTION: No. 6387644el motor proteins and methods for
; FILE REFERENCE: 1044
; CURRENT APPLICATION NUMBER: US/09/724,224
; CURRENT FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: 09/597,292
; PRIOR FILING DATE: 2000-06-20
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 370
; TYPE: PRT
; ORGANISM: Human
US-09-724-224-2

Query Match      62.0%; Score 49; DB 2; Length 370;
Best Local Similarity 66.7%; Pred. No. 0.71;
Matches 10; Conservative 2; Mismatches 3; Indels 3; Gaps 0;

Qy      1 RHYGETKNQSRSS 15
      | | | | | | | |
Db      232 RTVGATRLNQSRSS 246
      | | | | | | | |

RESULT 17
US-10-093-317-2
; Sequence 2, Application US/10093317
; Patent No. 6762043
; GENERAL INFORMATION:
; APPLICANT: Beraud, Christophe
; TITLE OF INVENTION: No. 6762043el motor proteins and methods for
; FILE REFERENCE: 1044
; CURRENT APPLICATION NUMBER: US/10/093,317
; CURRENT FILING DATE: 2002-03-06
; PRIOR APPLICATION NUMBER: 09/724,224
; PRIOR FILING DATE: 2000-11-28
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 370
; TYPE: PRT
; ORGANISM: Human
US-10-093-317-2

Query Match      62.0%; Score 49; DB 2; Length 370;
Best Local Similarity 66.7%; Pred. No. 0.71;
Matches 10; Conservative 2; Mismatches 3; Indels 3; Gaps 0;

Qy      1 RHYGETKNQSRSS 15
      | | | | | | | |
Db      232 RTVGATRLNQSRSS 246
      | | | | | | | |

RESULT 18
US-09-724-224-8
; Sequence 8, Application US/09724224
; Patent No. 6387644
; GENERAL INFORMATION:
; APPLICANT: Beraud, Christophe
; TITLE OF INVENTION: No. 6387644el motor proteins and methods for
; FILE REFERENCE: 1044
; CURRENT APPLICATION NUMBER: US/09/724,224
; CURRENT FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: 09/597,292
; PRIOR FILING DATE: 2000-06-20
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 487
; TYPE: PRT
; ORGANISM: Human
US-09-724-224-8

Query Match      62.0%; Score 49; DB 2; Length 487;
Best Local Similarity 66.7%; Pred. No. 0.96;
Matches 10; Conservative 2; Mismatches 3; Indels 3; Gaps 0;

Qy      1 RHYGETKNQSRSS 15
      | | | | | | | |
Db      208 RTVGATRLNQSRSS 222
      | | | | | | | |

RESULT 19
US-10-093-317-8
; Sequence 8, Application US/10093317
; Patent No. 6762043
; GENERAL INFORMATION:
; APPLICANT: Beraud, Christophe
; TITLE OF INVENTION: No. 6762043el motor proteins and methods for
; FILE REFERENCE: 1044
; CURRENT APPLICATION NUMBER: US/10/093,317
; CURRENT FILING DATE: 2002-03-06
; PRIOR APPLICATION NUMBER: 09/724,224
; PRIOR FILING DATE: 2000-11-28
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 487
; TYPE: PRT
; ORGANISM: Human
US-10-093-317-8

Query Match      62.0%; Score 49; DB 2; Length 487;
Best Local Similarity 66.7%; Pred. No. 0.96;
Matches 10; Conservative 2; Mismatches 3; Indels 3; Gaps 0;

Qy      1 RHYGETKNQSRSS 15
      | | | | | | | |
Db      208 RTVGATRLNQSRSS 222
      | | | | | | | |

RESULT 20
US-09-949-016-8784
; Sequence 8784, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
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```
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CLO01307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8784
; LENGTH: 490
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-8784

Query Match          62.0%; Score 49; DB 2; Length 490;
Best Local Similarity 66.7%; Pred. No. 0.96;
Matches 10; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY      1 RHYGETKNQSRSS 15
Db      240 RTVGATRLNQSRSS 254

RESULT 21
US-09-724-224-4
; Sequence 4, Application US/09724224
; Patent No. 6387644
; GENERAL INFORMATION:
; APPLICANT: Beraud, Christophe
; TITLE OF INVENTION: No. 6387644el motor proteins and methods for
; TITLE OF INVENTION: their use
; FILE REFERENCE: 1044
; CURRENT APPLICATION NUMBER: US/09/724,224
; CURRENT FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: 09/597,292
; PRIOR FILING DATE: 2000-06-20
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 512
; TYPE: PRT
; ORGANISM: Human
US-09-724-224-4

Query Match          62.0%; Score 49; DB 2; Length 512;
Best Local Similarity 66.7%; Pred. No. 1;
Matches 10; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY      1 RHYGETKNQSRSS 15
Db      233 RTVGATRLNQSRSS 247

RESULT 22
US-10-093-317-4
; Sequence 4, Application US/10093317
; Patent No. 6762043
; GENERAL INFORMATION:
; APPLICANT: Beraud, Christophe
; TITLE OF INVENTION: No. 6762043el motor proteins and methods for
; TITLE OF INVENTION: their use
; FILE REFERENCE: 1044
; CURRENT APPLICATION NUMBER: US/10/093,317
; CURRENT FILING DATE: 2002-03-06
; PRIOR APPLICATION NUMBER: 09/724,224
; PRIOR FILING DATE: 2000-11-28
; NUMBER OF SEQ ID NOS: 8
```

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; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 512
; TYPE: PRT
; ORGANISM: Human
US-10-093-317-4

Query Match          62.0%; Score 49; DB 2; Length 512;
Best Local Similarity 66.7%; Pred. No. 1;
Matches 10; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY      1 RHYGETKNQSRSS 15
Db      233 RTVGATRLNQSRSS 247

RESULT 23
US-09-595-684B-35
; Sequence 35, Application US/09595684B
; Patent No. 6544766
; GENERAL INFORMATION:
; APPLICANT: Beraud, Christophe
; APPLICANT: Ohashi, Cara
; APPLICANT: Sakowicz, Roman
; APPLICANT: Vaisberg, Eugeni
; APPLICANT: Wood, Kenneth
; APPLICANT: Yu, Ming
; TITLE OF INVENTION: Human kinesins and methods of producing
; TITLE OF INVENTION: and purifying human kinesins
; FILE REFERENCE: cytop036
; CURRENT APPLICATION NUMBER: US/09/595,684B
; CURRENT FILING DATE: 2002-06-24
; PRIOR APPLICATION NUMBER: 09/295,612
; PRIOR FILING DATE: 2000-04-20
; NUMBER OF SEQ ID NOS: 105
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 35
; LENGTH: 665
; TYPE: PRT
; ORGANISM: Human
US-09-595-684B-35

Query Match          62.0%; Score 49; DB 2; Length 665;
Best Local Similarity 66.7%; Pred. No. 1.3;
Matches 10; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY      1 RHYGETKNQSRSS 15
Db      232 RTVGATRLNQSRSS 246

RESULT 24
US-09-183-861-53
; Sequence 53, Application US/09183861
; Patent No. 6365165
; GENERAL INFORMATION:
; APPLICANT: Reed, Steven G.
; APPLICANT: Campos-Neto, Antonio
; APPLICANT: Webb, John R.
; APPLICANT: Dillon, Davin C.
; APPLICANT: Skelky, Yasir A.W.
; TITLE OF INVENTION: LEISHMANIA ANTIGENS FOR USEIN THE THERAPY AND
; NUMBER OF SEQUENCES: 87
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SEED and BERRY LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: USA
; ZIP: 98104-7092
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
```



```
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 53
; LENGTH: 324
; TYPE: PRT
; ORGANISM: Leishmania chagasi
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (1)...(324)
; OTHER INFORMATION: Xaa = Any Amino Acid
US-09-565-501A-53

Query Match          60.8%; Score 48; DB 2; Length 324;
Best Local Similarity 66.7%; Pred. No. 0.94;
Matches 10; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 RHYGETKMNQSRSS 15
Db 234 RHTAATKFNDRSS 248

RESULT 28
US-09-639-206A-53
; Sequence 53, Application US/09639206A
; Patent No. 661337
; GENERAL INFORMATION:
; APPLICANT: Reed, Steven G.
; APPLICANT: Campos-Neto, Antonio
; APPLICANT: Webb, John R.
; APPLICANT: Dillon, Davin C.
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Bhatia, Ajay
; APPLICANT: Coler, Rhea
; APPLICANT: Probst, Peter
; TITLE OF INVENTION: LEISHMANIA ANTIGENS FOR USE IN THE
; FILE REFERENCE: 210121.420C7
; CURRENT APPLICATION NUMBER: US/09/639,206A
; CURRENT FILING DATE: 2000-08-14
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 53
; LENGTH: 324
; TYPE: PRT
; ORGANISM: Leishmania chagasi
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (1)...(324)
; OTHER INFORMATION: Xaa = Any Amino Acid
US-09-639-206A-53

Query Match          60.8%; Score 48; DB 2; Length 324;
Best Local Similarity 66.7%; Pred. No. 0.94;
Matches 10; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 RHYGETKMNQSRSS 15
Db 234 RHTAATKFNDRSS 248

RESULT 29
US-09-874-923-53
; Sequence 53, Application US/09874923
; Patent No. 6638517
; GENERAL INFORMATION:
; APPLICANT: Reed, Steven G.
; APPLICANT: Campos-Neto, Antonio
; APPLICANT: Webb, John R.
; APPLICANT: Dillon, Davin C.
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Bhatia, Ajay
; APPLICANT: Coler, Rhea
; APPLICANT: Probst, Peter
; APPLICANT: Brannon, Mark
```

```
; TITLE OF INVENTION: LEISHMANIA ANTIGENS FOR USE IN THE
; FILE REFERENCE: 210121.420C8
; CURRENT APPLICATION NUMBER: US/09/874,923
; CURRENT FILING DATE: 2001-06-04
; NUMBER OF SEQ ID NOS: 122
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 53
; LENGTH: 324
; TYPE: PRT
; ORGANISM: Leishmania chagasi
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (1)...(324)
; OTHER INFORMATION: Xaa = Any Amino Acid
US-09-874-923-53

Query Match          60.8%; Score 48; DB 2; Length 324;
Best Local Similarity 66.7%; Pred. No. 0.94;
Matches 10; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 RHYGETKMNQSRSS 15
Db 234 RHTAATKFNDRSS 248

RESULT 30
US-08-713-815A-4
; Sequence 4, Application US/08713815A
; Patent No. 5830659
; GENERAL INFORMATION:
; APPLICANT: Russell J. Stewart
; TITLE OF INVENTION: ACTIVE MICROTUBULE-BASED
; SEPARATIONS BY KINESINS
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Thorpe, No. 5830659th & Western, L.L.P.
; STREET: 9035 South 700 East, Suite 200
; CITY: Sandy
; STATE: Utah
; COUNTRY: USA
; ZIP: 84070
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 inch, 1.44 Mb storage
; COMPUTER: AST Ascentia 900N
; OPERATING SYSTEM: DOS 6.22
; SOFTWARE: Word Perfect 6.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/713,815A
; FILING DATE: 13-SEP-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Alan J. Howarth
; REGISTRATION NUMBER: 36,553
; REFERENCE/DOCKET NUMBER: T3214/U-2202
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (801)566-6633
; TELEFAX: (801)566-0750
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 411 amino acid residues
; TYPE: amino acid
; TOPOLOGY: linear
US-08-713-815A-4

Query Match          57.0%; Score 45; DB 1; Length 411;
Best Local Similarity 60.0%; Pred. No. 4.2;
Matches 9; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 1 RHYGETKMNQSRSS 15
Db 197 RHIAVTNNHSSRS 211
```

```
RESULT 31
US-08-713-815A-3
; Sequence 3, Application US/08713815A
; Patent No. 5830659
; GENERAL INFORMATION:
; APPLICANT: Russell J. Stewart
; TITLE OF INVENTION: ACTIVE MICROTUBULE-BASED
; TITLE OF INVENTION: SEPARATIONS BY KINESINS
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Thorpe, No. 5830659th & Western, L.L.P.
; STREET: 9035 South 700 East, Suite 200
; CITY: Sandy
; STATE: Utah
; COUNTRY: USA
; ZIP: 84070
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 inch, 1.44 Mb storage
; COMPUTER: AST Ascentia 900N
; OPERATING SYSTEM: DOS 6.22
; SOFTWARE: Word Perfect 6.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/713,815A
; FILING DATE: 13-SEP-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Alan J. Howarth
; REGISTRATION NUMBER: 36,553
; REFERENCE/DOCKET NUMBER: T3214/U-2202
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (801)566-6633
; TELEFAX: (801)566-0750
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 441 amino acid residues
; TYPE: amino acid
; TOPOLOGY: linear
US-08-713-815A-3

Query Match 57.0%; Score 45; DB 1; Length 441;
Best Local Similarity 60.0%; Pred. No. 4.6;
Matches 9; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

Qy 1 RHYGETKMNQSRSS 15
Db 197 RHIAVTNNNEHSRS 211

RESULT 32
US-09-949-016-7425
; Sequence 7425, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7425
; LENGTH: 915
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-7425

Query Match 57.0%; Score 45; DB 1; Length 441;
Best Local Similarity 60.0%; Pred. No. 4.6;
Matches 9; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

Qy 1 RHYGETKMNQSRSS 15
Db 197 RHIAVTNNNEHSRS 211

RESULT 33
US-09-914-259-17
; Sequence 17, Application US/09914259
; Patent No. 6495336
; GENERAL INFORMATION:
; APPLICANT: Makowski, Lee
; APPLICANT: Hyman, Paul
; APPLICANT: Williams, Mark
; TITLE OF INVENTION: STAGED ASSEMBLY OF NANOSTRUCTURES
; FILE REFERENCE: 8471-010-999
; CURRENT APPLICATION NUMBER: US/09/914,259
; CURRENT FILING DATE: 2000-11-21
; NUMBER OF SEQ ID NOS: 180
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 17
; LENGTH: 956
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-914-259-17

Query Match 57.0%; Score 45; DB 2; Length 956;
Best Local Similarity 60.0%; Pred. No. 10;
Matches 9; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

Qy 1 RHYGETKMNQSRSS 15
Db 191 RHVAVTNNNEHSRS 205

RESULT 34
US-09-914-259-16
; Sequence 16, Application US/09914259
; Patent No. 6495336
; GENERAL INFORMATION:
; APPLICANT: Makowski, Lee
; APPLICANT: Hyman, Paul
; APPLICANT: Williams, Mark
; TITLE OF INVENTION: STAGED ASSEMBLY OF NANOSTRUCTURES
; FILE REFERENCE: 8471-010-999
; CURRENT APPLICATION NUMBER: US/09/914,259
; CURRENT FILING DATE: 2000-11-21
; NUMBER OF SEQ ID NOS: 180
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 16
; LENGTH: 957
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-914-259-16

Query Match 57.0%; Score 45; DB 2; Length 957;
Best Local Similarity 60.0%; Pred. No. 10;
Matches 9; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

Qy 1 RHYGETKMNQSRSS 15
Db 191 RHVAVTNNNEHSRS 205

RESULT 35
US-09-914-259-20
; Sequence 20, Application US/09914259
; Patent No. 6495336
; GENERAL INFORMATION:
```

```
; APPLICANT: Makowski, Lee
; APPLICANT: Hyman, Paul
; APPLICANT: Williams, Mark
; TITLE OF INVENTION: STAGED ASSEMBLY OF NANOSTRUCTURES
; FILE REFERENCE: 8471-010-999
; CURRENT APPLICATION NUMBER: US/09/914,259
; CURRENT FILING DATE: 2000-11-21
; NUMBER OF SEQ ID NOS: 180
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 20
; LENGTH: 963
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-914-259-20

Query Match      57.0%; Score 45; DB 2; Length 963;
Best Local Similarity 60.0%; Pred. No. 10;
Matches 9; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

Qy 1 RHYGETKNQRRSRS 15
Db 190 RHVAVTNMNEHSRS 204

RESULT 36
US-09-914-259-22
; Sequence 22, Application US/09914259
; Patent No. 6495336
; GENERAL INFORMATION:
; APPLICANT: Makowski, Lee
; APPLICANT: Hyman, Paul
; APPLICANT: Williams, Mark
; TITLE OF INVENTION: STAGED ASSEMBLY OF NANOSTRUCTURES
; FILE REFERENCE: 8471-010-999
; CURRENT APPLICATION NUMBER: US/09/914,259
; CURRENT FILING DATE: 2000-11-21
; NUMBER OF SEQ ID NOS: 180
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 21
; LENGTH: 967
; TYPE: PRT
; ORGANISM: Loligo pealeii
US-09-914-259-21

Query Match      57.0%; Score 45; DB 2; Length 967;
Best Local Similarity 60.0%; Pred. No. 11;
Matches 9; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

Qy 1 RHYGETKNQRRSRS 15
Db 190 RHVAVTNMNEHSRS 204

RESULT 39
US-09-914-259-19
; Sequence 19, Application US/09914259
; Patent No. 6495336
; GENERAL INFORMATION:
; APPLICANT: Makowski, Lee
; APPLICANT: Hyman, Paul
; APPLICANT: Williams, Mark
; TITLE OF INVENTION: STAGED ASSEMBLY OF NANOSTRUCTURES
; FILE REFERENCE: 8471-010-999
; CURRENT APPLICATION NUMBER: US/09/914,259
; CURRENT FILING DATE: 2000-11-21
; NUMBER OF SEQ ID NOS: 180
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 19
; LENGTH: 975
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
US-09-914-259-19

Query Match      57.0%; Score 45; DB 2; Length 975;
Best Local Similarity 60.0%; Pred. No. 11;
Matches 9; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

Qy 1 RHYGETKNQRRSRS 15
Db 197 RHVAVTNMNEHSRS 211
```

```
; APPLICANT: Makowski, Lee
; APPLICANT: Hyman, Paul
; APPLICANT: Williams, Mark
; TITLE OF INVENTION: STAGED ASSEMBLY OF NANOSTRUCTURES
; FILE REFERENCE: 8471-010-999
; CURRENT APPLICATION NUMBER: US/09/914,259
; CURRENT FILING DATE: 2000-11-21
; NUMBER OF SEQ ID NOS: 180
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 20
; LENGTH: 963
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-914-259-20

Query Match      57.0%; Score 45; DB 2; Length 963;
Best Local Similarity 60.0%; Pred. No. 10;
Matches 9; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

Qy 1 RHYGETKNQRRSRS 15
Db 190 RHVAVTNMNEHSRS 204

RESULT 36
US-09-914-259-22
; Sequence 22, Application US/09914259
; Patent No. 6495336
; GENERAL INFORMATION:
; APPLICANT: Makowski, Lee
; APPLICANT: Hyman, Paul
; APPLICANT: Williams, Mark
; TITLE OF INVENTION: STAGED ASSEMBLY OF NANOSTRUCTURES
; FILE REFERENCE: 8471-010-999
; CURRENT APPLICATION NUMBER: US/09/914,259
; CURRENT FILING DATE: 2000-11-21
; NUMBER OF SEQ ID NOS: 180
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 22
; LENGTH: 963
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-914-259-22

Query Match      57.0%; Score 45; DB 2; Length 963;
Best Local Similarity 60.0%; Pred. No. 10;
Matches 9; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

Qy 1 RHYGETKNQRRSRS 15
Db 190 RHVAVTNMNEHSRS 204

RESULT 37
US-09-538-092-1060
; Sequence 1060, Application US/09538092
; Patent No. 6753314
; GENERAL INFORMATION:
; APPLICANT: Mansfield, Traci A.
; APPLICANT: Giot, Loic
; TITLE OF INVENTION: Protein-Protein Complexes and Method of Using Same
; FILE REFERENCE: 15966-542
; CURRENT APPLICATION NUMBER: US/09/538,092
; CURRENT FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: 60/127,352
; PRIOR FILING DATE: 1999-04-01
; PRIOR APPLICATION NUMBER: 60/178,965
; PRIOR FILING DATE: 2000-02-01
; NUMBER OF SEQ ID NOS: 1387
; SOFTWARE: CuraPatSeqFormatter Version 0.9
; SEQ ID NO 1060
; LENGTH: 963
; TYPE: PRT
```

```
RESULT 40
US-09-949-016-10196
; Sequence 10196, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10196
; LENGTH: 978
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-10196

Query Match          57.0%; Score 45; DB 2; Length 978;
Best Local Similarity 60.0%; Pred. No. 11;
Matches 9; Conservative 1; Mismatches 5; Indels 5; Gaps 0;

Qy 1 RHYGETKNQSRSS 15
|||:||||
Db 205 RHVAVTNMNEHSRS 219

RESULT 41
US-09-914-259-27
; Sequence 27, Application US/09914259
; Patent No. 6495336
; GENERAL INFORMATION:
; APPLICANT: Makowski, Lee
; APPLICANT: Hyman, Paul
; APPLICANT: Williams, Mark
; TITLE OF INVENTION: STAGED ASSEMBLY OF NANOSTRUCTURES
; FILE REFERENCE: 8471-010-999
; CURRENT APPLICATION NUMBER: US/09/914,259
; CURRENT FILING DATE: 2000-11-21
; NUMBER OF SEQ ID NOS: 180
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 27
; LENGTH: 1027
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-914-259-27

Query Match          57.0%; Score 45; DB 2; Length 1027;
Best Local Similarity 60.0%; Pred. No. 11;
Matches 9; Conservative 1; Mismatches 5; Indels 5; Gaps 0;

Qy 1 RHYGETKNQSRSS 15
|||:||||
Db 191 RHVAVTNMNEHSRS 205

RESULT 42
US-09-914-259-24
; Sequence 24, Application US/09914259
; Patent No. 6495336
; GENERAL INFORMATION:
; APPLICANT: Makowski, Lee
; APPLICANT: Hyman, Paul
; APPLICANT: Williams, Mark
; TITLE OF INVENTION: STAGED ASSEMBLY OF NANOSTRUCTURES
```

```
; FILE REFERENCE: 8471-010-999
; CURRENT APPLICATION NUMBER: US/09/914,259
; CURRENT FILING DATE: 2000-11-21
; NUMBER OF SEQ ID NOS: 180
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 24
; LENGTH: 1031
; TYPE: PRT
; ORGANISM: Strongylocentrotus purpuratus
US-09-914-259-24

Query Match          57.0%; Score 45; DB 2; Length 1031;
Best Local Similarity 60.0%; Pred. No. 11;
Matches 9; Conservative 1; Mismatches 5; Indels 5; Gaps 0;

Qy 1 RHYGETKNQSRSS 15
|||:||||
Db 189 RHVAVTNMNEHSRS 203

RESULT 43
US-09-914-259-26
; Sequence 26, Application US/09914259
; Patent No. 6495336
; GENERAL INFORMATION:
; APPLICANT: Makowski, Lee
; APPLICANT: Hyman, Paul
; APPLICANT: Williams, Mark
; TITLE OF INVENTION: STAGED ASSEMBLY OF NANOSTRUCTURES
; FILE REFERENCE: 8471-010-999
; CURRENT APPLICATION NUMBER: US/09/914,259
; CURRENT FILING DATE: 2000-11-21
; NUMBER OF SEQ ID NOS: 180
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 26
; LENGTH: 1032
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-914-259-26

Query Match          57.0%; Score 45; DB 2; Length 1032;
Best Local Similarity 60.0%; Pred. No. 11;
Matches 9; Conservative 1; Mismatches 5; Indels 5; Gaps 0;

Qy 1 RHYGETKNQSRSS 15
|||:||||
Db 191 RHVAVTNMNEHSRS 205

RESULT 44
US-09-538-092-1293
; Sequence 1293, Application US/09538092
; Patent No. 6753314
; GENERAL INFORMATION:
; APPLICANT: Giot, Loic
; APPLICANT: Mansfield, Traci A.
; TITLE OF INVENTION: Protein-Protein Complexes and Method of Using Same
; FILE REFERENCE: 15966-542
; CURRENT APPLICATION NUMBER: US/09/538,092
; CURRENT FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: 60/127,352
; PRIOR FILING DATE: 1999-04-01
; PRIOR APPLICATION NUMBER: 60/178,965
; PRIOR FILING DATE: 2000-02-01
; NUMBER OF SEQ ID NOS: 1387
; SOFTWARE: CuraPatSeqformatter Version 0.9
; SEQ ID NO 1293
; LENGTH: 1032
; TYPE: PRT
; ORGANISM: Homo sapiens
; APPLICANT: Makowski, Lee
; APPLICANT: Hyman, Paul
; APPLICANT: Williams, Mark
; NAME/KEY: misc feature
; LOCATION: (0)...(0)
```



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; OTHER INFORMATION: Polypeptide Accession Number Q12840
US-09-538-092-1293

Query Match          57.0%; Score 45; DB 2; Length 1032;
Best Local Similarity 60.0%; Pred. No. 11;
Matches 9; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 1 RHYGETKNQRRSSRS 15
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Db 191 RHVAVTNMEHSRS 205

RESULT 45
US-09-252-991A-26189
; Sequence 26189, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 26189
; LENGTH: 683
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-26189

Query Match          55.7%; Score 44; DB 2; Length 683;
Best Local Similarity 53.3%; Pred. No. 11;
Matches 8; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 RHYGETKNQRRSSRS 15
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Db 176 RHRGTGROGRRS 190

RESULT 46
US-09-914-259-29
; Sequence 29, Application US/09914259
; Patent No. 6495336
; GENERAL INFORMATION:
; APPLICANT: Hyman, Paul
; APPLICANT: Williams, Mark
; TITLE OF INVENTION: STAGED ASSEMBLY OF NANOSTRUCTURES
; FILE REFERENCE: 8471-010-999
; CURRENT APPLICATION NUMBER: US/09/914,259
; CURRENT FILING DATE: 2000-11-21
; NUMBER OF SEQ ID NOS: 180
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 29
; LENGTH: 706
; TYPE: PRT
; ORGANISM: Saccharomyces cerevisiae
US-09-914-259-29

Query Match          55.7%; Score 44; DB 2; Length 706;
Best Local Similarity 66.7%; Pred. No. 11;
Matches 10; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 RHYGETKNQRRSSRS 15
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Db 330 RKIGETDYNARRSS 344

RESULT 47
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US-09-641-806-4
; Sequence 4, Application US/09641806
; Patent No. 6395527
; GENERAL INFORMATION:
; APPLICANT: Beraud, Christophe
; APPLICANT: Freedman, Richard
; TITLE OF INVENTION: No. 6395527el motor proteins and methods for
; TITLE OF INVENTION: their use
; FILE REFERENCE: 1034
; CURRENT APPLICATION NUMBER: US/09/641,806
; CURRENT FILING DATE: 2000-08-17
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 337
; TYPE: PRT
; ORGANISM: Human
US-09-641-806-4

Query Match          54.4%; Score 43; DB 2; Length 337;
Best Local Similarity 60.0%; Pred. No. 7.9;
Matches 9; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 1 RHYGETKNQRRSSRS 15
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Db 190 RHTGATHLNHLSSRS 204

RESULT 48
US-09-723-129-4
; Sequence 4, Application US/09723129
; Patent No. 6551787
; GENERAL INFORMATION:
; APPLICANT: Beraud, Christophe
; APPLICANT: Freedman, Richard
; TITLE OF INVENTION: No. 6551787el motor proteins and methods for
; TITLE OF INVENTION: their use
; FILE REFERENCE: 1034
; CURRENT APPLICATION NUMBER: US/09/723,129
; CURRENT FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 09/641,806
; PRIOR FILING DATE: 2000-08-17
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 337
; TYPE: PRT
; ORGANISM: Human
US-09-723-129-4

Query Match          54.4%; Score 43; DB 2; Length 337;
Best Local Similarity 60.0%; Pred. No. 7.9;
Matches 9; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 1 RHYGETKNQRRSSRS 15
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Db 190 RHTGATHLNHLSSRS 204

RESULT 49
US-09-722-862-4
; Sequence 4, Application US/09722862
; Patent No. 6562610
; GENERAL INFORMATION:
; APPLICANT: Beraud, Christophe
; APPLICANT: Freedman, Richard
; TITLE OF INVENTION: No. 6562610el motor proteins and methods for
; TITLE OF INVENTION: their use
; FILE REFERENCE: 1034
; CURRENT APPLICATION NUMBER: US/09/722,862
; CURRENT FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 09/641,806
; PRIOR FILING DATE: 2000-08-17
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; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 337
; TYPE: PRT
; ORGANISM: Human
US-09-722-862-4

Query Match 54.4%; Score 43; DB 2; Length 337;
Best Local Similarity 60.0%; Pred. No. 7.9;
Matches 9; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

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Db 190 RHTGATHLNLSSRS 204

RESULT 50
US-09-641-806-2
; Sequence 2, Application US/09641806
; Patent No. 6395527
; GENERAL INFORMATION:
; APPLICANT: Beraud, Christophe
; APPLICANT: Freedman, Richard
; TITLE OF INVENTION: No. 6395527el motor proteins and methods for
; TITLE OF INVENTION: their use
; FILE REFERENCE: 1034
; CURRENT APPLICATION NUMBER: US/09/641,806
; CURRENT FILING DATE: 2000-08-17
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 342
; TYPE: PRT
; ORGANISM: Human
US-09-641-806-2

Query Match 54.4%; Score 43; DB 2; Length 342;
Best Local Similarity 60.0%; Pred. No. 8;
Matches 9; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

Qy 1 RHYGETKMQRSRS 15
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Db 191 RHTGATHLNLSSRS 205

Search completed: April 21, 2006, 13:43:19
Job time : 56 secs

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OM protein - protein search, using sw model

Run on: April 21, 2006, 13:53:21 ; Search time 164 Seconds
(without alignments)
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Title: US-09-993-399-1

Perfect score: 79

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Listing first 1000 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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3	79	100.0	2503	US-10-828-985A-11	Sequence 11, Appli
4	79	100.0	2543	US-10-828-985A-9	Sequence 9, Appli
5	79	100.0	2568	US-10-828-985A-7	Sequence 7, Appli
6	79	100.0	2633	US-10-450-763-36864	Sequence 36864, A
7	79	100.0	2663	US-10-723-860-749	Sequence 749, App
8	69	87.3	2954	US-10-650-280-1	Sequence 1, Appli
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10	65	82.3	694	US-10-425-114-59725	Sequence 59725, A
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12	53	67.1	2013	US-10-097-143-13758	Sequence 13758, A
13	52	65.8	154	US-09-864-408A-1218	Sequence 1218, Ap
14	52	65.8	1382	US-10-437-963-176714	Sequence 176714, A
15	52	65.8	1401	US-10-287-226-142	Sequence 142, App
16	52	65.8	1931	US-10-097-143-9828	Sequence 9828, Ap
17	51	64.6	197	US-10-425-115-245875	Sequence 245875, A
18	50	63.3	677	US-11-097-143-22341	Sequence 22341, A
19	49	62.0	259	US-10-425-115-210540	Sequence 210540, A
20	49	62.0	346	US-10-797-893-6	Sequence 6, Appli
21	49	62.0	370	US-10-797-893-2	Sequence 2, Appli
22	49	62.0	460	US-09-925-300-1228	Sequence 1228, Ap
23	49	62.0	487	US-10-797-893-8	Sequence 8, Appli
24	49	62.0	490	US-10-334-143-80	Sequence 80, Appli
25	49	62.0	512	US-10-797-893-4	Sequence 4, Appli
26	49	62.0	665	US-10-733-878-425	Sequence 425, App
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31	48	60.8	906	4	US-10-437-963-163527	Sequence 163527, A
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33	47	59.5	75	4	US-10-424-599-152360	Sequence 152360, A
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51	45	57.0	956	4	US-10-370-685-106	Sequence 106, App
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53	45	57.0	957	4	US-10-370-685-105	Sequence 105, App
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55	45	57.0	963	4	US-10-080-608A-22	Sequence 22, Appli
56	45	57.0	963	4	US-10-370-685-109	Sequence 109, App
57	45	57.0	963	4	US-10-370-685-111	Sequence 111, App
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59	45	57.0	967	4	US-10-080-608A-21	Sequence 21, Appli
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61	45	57.0	975	4	US-10-080-608A-19	Sequence 19, Appli
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67	45	57.0	1027	4	US-10-370-685-116	Sequence 116, App
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81	44	55.7	451	4	US-10-425-115-344989	Sequence 344989, A
82	44	55.7	706	4	US-10-080-608A-29	Sequence 29, Appli
83	44	55.7	706	4	US-10-370-685-118	Sequence 118, App
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91	44	55.7	966	4	US-10-425-114-62697	Sequence 62697, A
92	44	55.7	1147	4	US-10-437-963-104637	Sequence 104637, A
93	44	55.7	1462	4	US-10-437-963-158098	Sequence 158098, A
94	43	54.4	169	4	US-10-424-599-158452	Sequence 158452, A
95	43	54.4	672	4	US-10-408-765A-1664	Sequence 1664, Ap
96	43	54.4	915	4	US-10-437-963-112350	Sequence 112350, A
97	43	54.4	950	4	US-10-425-115-247543	Sequence 247543, A
98	43	54.4	954	4	US-10-473-276-2	Sequence 2, Appli
99	43	54.4	954	4	US-10-425-114-62672	Sequence 62672, A
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101	43	54.4	1004	4	US-10-473-276-3	Sequence 3, Appli	174	38	48.1	190	5	US-10-723-860-379	Sequence 379, App
102	43	54.4	1062	4	US-10-195-144-37	Sequence 37, Appl	175	38	48.1	190	5	US-10-489-125B-7	Sequence 7, Appli
103	43	54.4	1062	4	US-10-345-072-37	Sequence 37, Appl	176	38	48.1	215	4	US-10-221-625-88	Sequence 88, Appl
104	43	54.4	1324	4	US-10-287-226-314	Sequence 314, App	177	38	48.1	218	4	US-10-424-599-192104	Sequence 192104,
105	42	53.2	154	4	US-10-424-599-274030	Sequence 274030, A	178	38	48.1	231	4	US-10-425-115-284664	Sequence 284664,
106	42	53.2	214	4	US-10-425-115-43702	Sequence 43702, A	179	38	48.1	265	4	US-10-424-599-149745	Sequence 149745,
107	42	53.2	238	4	US-10-425-115-190347	Sequence 190347, A	180	38	48.1	299	4	US-10-282-122A-47532	Sequence 47532, A
108	42	53.2	326	4	US-10-432-424-4	Sequence 4, Appli	181	38	48.1	323	4	US-10-425-114-65066	Sequence 65066, A
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110	42	53.2	517	4	US-10-369-493-12881	Sequence 12881, A	183	38	48.1	334	5	US-10-489-125B-5	Sequence 5, Appli
111	42	53.2	569	4	US-10-425-115-321707	Sequence 321707, A	184	38	48.1	335	4	US-10-425-114-41908	Sequence 41908, A
112	42	53.2	676	4	US-10-425-114-43723	Sequence 43723, A	185	38	48.1	346	4	US-10-156-761-13468	Sequence 13468, A
113	42	53.2	787	4	US-10-432-424-2	Sequence 2, Appli	186	38	48.1	375	4	US-10-332-089-4	Sequence 4, Appli
114	42	53.2	1006	4	US-10-437-963-147933	Sequence 147933, A	187	38	48.1	409	4	US-10-332-089-6	Sequence 6, Appli
115	42	53.2	1022	4	US-10-437-963-133108	Sequence 133108, A	188	38	48.1	455	4	US-10-437-963-195620	Sequence 195620,
116	42	53.2	1197	4	US-10-425-115-190351	Sequence 190351, A	189	38	48.1	463	6	US-11-097-143-38796	Sequence 38796, A
117	42	53.2	1218	6	US-11-097-143-30399	Sequence 30399, A	190	38	48.1	484	4	US-10-425-115-347146	Sequence 347146, A
118	41	51.9	138	4	US-10-425-115-254409	Sequence 254409, A	191	38	48.1	505	4	US-10-425-114-51793	Sequence 51793, A
119	41	51.9	175	3	US-09-898-659-17	Sequence 17, Appl	192	38	48.1	515	4	US-10-425-114-70647	Sequence 70647, A
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131	41	51.9	788	4	US-10-369-493-3863	Sequence 3863, Ap	204	38	48.1	1388	4	US-10-424-599-258016	Sequence 258016,
132	41	51.9	875	4	US-10-425-115-348360	Sequence 348360, A	205	38	48.1	1388	4	US-10-146-473-82	Sequence 82, Appl
133	41	51.9	1014	4	US-10-437-963-156793	Sequence 156793, A	206	38	48.1	1388	4	US-10-173-999-32	Sequence 32, Appl
134	41	51.9	1045	4	US-10-437-963-150217	Sequence 150217, A	207	38	48.1	1388	4	US-10-332-089-2	Sequence 2, Appli
135	41	51.9	1080	4	US-10-437-963-142399	Sequence 142399, A	208	38	48.1	1388	4	US-10-188-832-164	Sequence 164, App
136	41	51.9	1252	4	US-10-437-963-129734	Sequence 129734, A	209	38	48.1	1388	5	US-10-733-878-411	Sequence 411, App
137	40	50.6	160	3	US-09-833-245-426	Sequence 426, App	210	38	48.1	1388	5	US-10-723-860-2948	Sequence 2948, Ap
138	40	50.6	201	4	US-10-425-115-209860	Sequence 209860, A	211	37	46.8	48	4	US-10-425-115-196590	Sequence 196590,
139	40	50.6	302	3	US-09-738-626-6862	Sequence 6862, Ap	212	37	46.8	57	4	US-10-425-115-257192	Sequence 257192,
140	40	50.6	401	4	US-10-108-260A-3987	Sequence 3987, Ap	213	37	46.8	78	4	US-10-424-599-239433	Sequence 239433,
141	40	50.6	784	6	US-11-097-143-40128	Sequence 40128, A	214	37	46.8	83	4	US-10-425-115-185388	Sequence 185388,
142	40	50.6	835	4	US-10-437-963-135715	Sequence 135715, A	215	37	46.8	85	4	US-10-767-701-56670	Sequence 56670, A
143	40	50.6	916	4	US-10-287-226-330	Sequence 330, App	216	37	46.8	87	4	US-10-267-502-297	Sequence 297, App
144	40	50.6	1003	6	US-11-097-143-11007	Sequence 11007, A	217	37	46.8	87	6	US-11-097-143-21912	Sequence 21912, A
145	40	50.6	1142	4	US-10-369-493-1700	Sequence 1700, Ap	218	37	46.8	101	4	US-10-425-115-253127	Sequence 253127,
146	40	50.6	1142	4	US-10-618-581-10	Sequence 10, Appl	219	37	46.8	107	4	US-10-425-115-253127	Sequence 253127,
147	40	50.6	1248	4	US-10-437-963-169178	Sequence 169178, A	220	37	46.8	137	4	US-10-062-467A-3	Sequence 3, Appli
148	39	49.4	157	4	US-10-424-599-195574	Sequence 195574, A	221	37	46.8	159	3	US-09-451-322-26	Sequence 26, Appl
149	39	49.4	225	4	US-10-158-160A-13	Sequence 13, Appl	222	37	46.8	159	4	US-10-372-614-26	Sequence 26, Appl
150	39	49.4	292	4	US-10-158-160A-11	Sequence 11, Appl	223	37	46.8	159	4	US-10-374-603-26	Sequence 26, Appl
151	39	49.4	451	4	US-10-282-122A-47340	Sequence 47340, A	224	37	46.8	159	5	US-10-958-062-26	Sequence 26, Appl
152	39	49.4	624	4	US-10-767-701-44549	Sequence 44549, A	225	37	46.8	179	4	US-10-767-701-53097	Sequence 53097, A
153	39	49.4	884	3	US-09-741-150-4	Sequence 4, Appli	226	37	46.8	209	5	US-10-450-763-33491	Sequence 33491, A
154	39	49.4	884	5	US-10-612-012-4	Sequence 4, Appli	227	37	46.8	233	4	US-10-425-115-363311	Sequence 363311,
155	39	49.4	885	4	US-10-156-239-47	Sequence 47, Appl	228	37	46.8	240	4	US-10-437-963-152398	Sequence 152398,
156	39	49.4	887	5	US-10-739-930-10838	Sequence 10838, A	229	37	46.8	260	4	US-10-425-115-195040	Sequence 195040,
157	39	49.4	922	4	US-10-437-963-125036	Sequence 125036, A	230	37	46.8	297	4	US-10-425-115-283055	Sequence 283055,
158	39	49.4	928	4	US-10-080-608A-23	Sequence 23, Appl	231	37	46.8	329	4	US-10-311-642-4	Sequence 4, Appli
159	39	49.4	928	4	US-10-370-685-112	Sequence 112, App	232	37	46.8	406	4	US-10-369-493-3789	Sequence 3789, Ap
160	39	49.4	932	4	US-10-369-493-6025	Sequence 6025, Ap	233	37	46.8	427	4	US-10-425-115-277547	Sequence 277547,
161	39	49.4	1038	4	US-10-369-493-1708	Sequence 1708, Ap	234	37	46.8	431	4	US-10-182-243-48	Sequence 48, Appl
162	38	48.7	297	5	US-10-450-763-51623	Sequence 51623, A	235	37	46.8	445	4	US-10-282-122A-49547	Sequence 49547, A
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164	38	48.1	79	4	US-10-425-115-354606	Sequence 354606, A	237	37	46.8	505	4	US-10-424-599-149866	Sequence 149866,
165	38	48.1	87	4	US-10-425-115-205098	Sequence 205098, A	238	37	46.8	528	4	US-10-173-999-103	Sequence 103, App
166	38	48.1	114	4	US-10-437-963-187430	Sequence 187430, A	239	37	46.8	539	4	US-10-156-761-11731	Sequence 11731, A
167	38	48.1	114	4	US-10-425-115-236961	Sequence 236961, A	240	37	46.8	545	4	US-10-029-386-33143	Sequence 33143, A
168	38	48.1	157	4	US-10-424-599-201597	Sequence 201597, A	241	37	46.8	602	4	US-10-369-493-23667	Sequence 23667, A
169	38	48.1	166	3	US-09-764-864-1153	Sequence 1153, Ap	242	37	46.8	627	4	US-10-025-145A-32	Sequence 32, Appl
170	38	48.1	168	4	US-10-437-963-158837	Sequence 158837, A	243	37	46.8	729	6	US-11-097-143-5292	Sequence 5292, Ap
171	38	48.1	176	4	US-10-424-599-175098	Sequence 175098, A	244	37	46.8	811	4	US-10-144-194A-26	Sequence 26, Appl
172	38	48.1	187	4	US-10-437-963-190040	Sequence 190040, A	245	37	46.8	811	4	US-10-144-194A-98	Sequence 98, Appl
173	38	48.1	190	4	US-10-158-160A-16	Sequence 16, Appl	246	37	46.8	811	5	US-10-431-566-26	Sequence 26, Appl

247	37	46.8	811	5	US-10-491-566-98	Sequence 98, Appl	320	36	45.6	671	4	US-10-425-115-259713	Sequence 259713,
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249	37	46.8	850	4	US-10-437-963-186016	Sequence 186016,	322	36	45.6	695	4	US-10-437-963-176889	Sequence 176889,
250	37	46.8	884	4	US-10-250-889-79	Sequence 79, Appl	323	36	45.6	696	4	US-10-408-765A-1067	Sequence 1067, Ap
251	37	46.8	890	4	US-10-171-311-136	Sequence 196, App	324	36	45.6	702	4	US-10-425-115-223635	Sequence 223635,
252	37	46.8	890	5	US-10-733-878-459	Sequence 459, App	325	36	45.6	749	4	US-10-425-114-70823	Sequence 70823, A
253	37	46.8	890	5	US-10-737-450-14	Sequence 14, Appl	326	36	45.6	749	4	US-10-220-120-366	Sequence 366, App
254	37	46.8	923	4	US-10-437-963-182305	Sequence 182305,	327	36	45.6	757	4	US-10-363-829-316	Sequence 316, App
255	37	46.8	960	3	US-09-734-426-1	Sequence 1, Appl	328	36	45.6	782	4	US-10-276-774-1718	Sequence 1718, Ap
256	37	46.8	960	4	US-10-264-885-1	Sequence 1, Appl	329	36	45.6	794	4	US-10-425-115-285510	Sequence 285510,
257	37	46.8	993	5	US-10-723-860-1832	Sequence 1832, Ap	330	36	45.6	803	5	US-10-840-060-143	Sequence 143, App
258	37	46.8	1016	4	US-10-753-901-16	Sequence 16, Appl	331	36	45.6	803	6	US-11-097-143-1104	Sequence 1104, Ap
259	37	46.8	1016	4	US-10-754-115-16	Sequence 16, Appl	332	36	45.6	888	4	US-10-425-115-251250	Sequence 251250, A
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263	37	46.8	1274	6	US-11-018-067-1	Sequence 1, Appl	336	36	45.6	1175	4	US-10-694-711-8	Sequence 7118, Ap
264	37	46.8	1437	4	US-10-437-963-189430	Sequence 189430,	337	36	45.6	1224	4	US-10-424-599-251293	Sequence 251293,
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266	37	46.8	1830	4	US-10-437-963-189860	Sequence 189860,	339	36	45.6	1271	4	US-10-437-963-103408	Sequence 103408,
267	37	46.8	3138	6	US-11-097-143-18666	Sequence 18666, A	340	36	45.6	1362	4	US-10-296-838-2	Sequence 2, Appl
268	36.5	46.2	247	5	US-10-450-763-53521	Sequence 53521, A	341	36	45.6	1826	4	US-10-408-765A-1477	Sequence 1477, Ap
269	36	45.6	57	4	US-10-424-599-259723	Sequence 259723,	342	35	44.9	456	6	US-11-097-143-25710	Sequence 25710, A
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272	36	45.6	74	4	US-10-424-599-279780	Sequence 279780,	345	35	44.3	89	4	US-10-424-599-251563	Sequence 251563,
273	36	45.6	75	4	US-10-424-599-150984	Sequence 150984,	346	35	44.3	108	4	US-10-425-115-262998	Sequence 262998,
274	36	45.6	77	4	US-10-156-761-8517	Sequence 8517, Ap	347	35	44.3	114	4	US-10-424-599-215715	Sequence 215715,
275	36	45.6	79	4	US-10-724-972A-4061	Sequence 4061, Ap	348	35	44.3	117	5	US-10-450-763-50902	Sequence 50902, A
276	36	45.6	88	4	US-10-424-599-246121	Sequence 246121,	349	35	44.3	122	4	US-10-238-075-1540	Sequence 1540, Ap
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278	36	45.6	159	4	US-10-437-963-186465	Sequence 186465,	351	35	44.3	137	4	US-10-101-464A-669	Sequence 669, App
279	36	45.6	161	4	US-10-767-701-32708	Sequence 32708, A	352	35	44.3	137	5	US-10-864-252-669	Sequence 669, App
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281	36	45.6	182	4	US-10-437-963-156985	Sequence 156985,	354	35	44.3	162	6	US-11-097-143-5985	Sequence 5985, Ap
282	36	45.6	183	4	US-10-767-701-32202	Sequence 32202, A	355	35	44.3	165	4	US-10-238-075-773	Sequence 773, App
283	36	45.6	211	4	US-10-767-701-45409	Sequence 45409, A	356	35	44.3	165	4	US-10-425-114-67907	Sequence 67907, A
284	36	45.6	248	3	US-09-791-171-60	Sequence 60, Appl	357	35	44.3	167	4	US-10-425-115-227602	Sequence 227602,
285	36	45.6	248	3	US-09-804-980-60	Sequence 60, Appl	358	35	44.3	168	4	US-10-369-493-18405	Sequence 18405, A
286	36	45.6	248	4	US-10-620-246-60	Sequence 60, Appl	359	35	44.3	174	4	US-10-437-963-177646	Sequence 177646,
287	36	45.6	257	4	US-10-425-115-284665	Sequence 284665,	360	35	44.3	180	4	US-10-767-701-40263	Sequence 40263, A
288	36	45.6	262	4	US-10-156-761-11272	Sequence 11272, A	361	35	44.3	190	4	US-10-767-701-34271	Sequence 34271, A
289	36	45.6	262	4	US-10-156-761-11523	Sequence 11523, A	362	35	44.3	194	3	US-09-774-639-242	Sequence 242, App
290	36	45.6	299	4	US-10-282-122A-50463	Sequence 50463, A	363	35	44.3	194	3	US-09-969-730-341	Sequence 341, App
291	36	45.6	312	4	US-10-424-599-260604	Sequence 260604,	364	35	44.3	194	4	US-10-621-363-341	Sequence 341, App
292	36	45.6	313	5	US-10-733-923-1441	Sequence 1441, Ap	365	35	44.3	198	4	US-10-437-963-181203	Sequence 181203,
293	36	45.6	317	4	US-10-144-156-12	Sequence 12, Appl	366	35	44.3	203	4	US-10-424-599-182148	Sequence 182148,
294	36	45.6	321	4	US-10-238-075-1147	Sequence 1147, Ap	367	35	44.3	221	4	US-10-424-599-232532	Sequence 232532,
295	36	45.6	352	4	US-10-296-838-4	Sequence 4, Appl	368	35	44.3	237	5	US-10-450-763-31586	Sequence 31586, A
296	36	45.6	372	4	US-10-424-599-155654	Sequence 155654,	369	35	44.3	250	4	US-10-450-763-54197	Sequence 54197, A
297	36	45.6	375	5	US-10-987-454-106	Sequence 106, App	370	35	44.3	254	4	US-10-425-115-251693	Sequence 251693,
298	36	45.6	384	3	US-09-803-285-2	Sequence 2, Appl	371	35	44.3	281	5	US-10-420-345A-11	Sequence 11, Appl
299	36	45.6	384	4	US-10-291-337-2	Sequence 2, Appl	372	35	44.3	284	5	US-10-739-930-8910	Sequence 8910, Ap
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301	36	45.6	401	4	US-10-080-170-182	Sequence 182, App	374	35	44.3	299	4	US-10-437-963-134586	Sequence 134586,
302	36	45.6	401	4	US-10-468-356-182	Sequence 182, App	375	35	44.3	306	3	US-09-726-643-73	Sequence 73, Appl
303	36	45.6	406	4	US-10-424-599-276516	Sequence 276516,	376	35	44.3	306	4	US-10-042-141-73	Sequence 73, Appl
304	36	45.6	421	6	US-11-097-143-38148	Sequence 38148, A	377	35	44.3	306	5	US-10-919-272-73	Sequence 73, Appl
305	36	45.6	433	4	US-10-425-114-47964	Sequence 47964, A	378	35	44.3	308	4	US-10-425-114-60021	Sequence 60021, A
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308	36	45.6	463	4	US-10-425-115-295253	Sequence 295253,	381	35	44.3	323	4	US-10-425-114-40690	Sequence 40690, A
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311	36	45.6	475	4	US-10-425-114-50971	Sequence 50971, A	384	35	44.3	340	3	US-09-861-014-9	Sequence 9, Appl
312	36	45.6	577	4	US-10-425-115-232694	Sequence 232694,	385	35	44.3	340	3	US-10-283-359-1	Sequence 1, Appl
313	36	45.6	581	5	US-10-739-736-3	Sequence 3, Appl	386	35	44.3	340	4	US-10-191-698-1	Sequence 1, Appl
314	36	45.6	583	4	US-10-282-122A-77634	Sequence 77634, A	387	35	44.3	340	4	US-10-420-529-5	Sequence 5, Appl
315	36	45.6	587	6	US-10-437-963-194304	Sequence 194304,	388	35	44.3	340	4	US-10-420-529-20	Sequence 20, Appl
316	36	45.6	626	6	US-11-097-143-5991	Sequence 5991, Ap	389	35	44.3	340	4	US-10-420-529-21	Sequence 21, Appl
317	36	45.6	666	4	US-10-425-114-54408	Sequence 54408, A	390	35	44.3	340	4	US-10-608-516-1	Sequence 1, Appl
318	36	45.6	667	4	US-10-425-114-69034	Sequence 69034, A	391	35	44.3	340	5	US-10-861-108-1	Sequence 1, Appl
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393	35	44.3	370	5	US-10-450-763-54201	Sequence 54201, A	466	35	44.3	632	3	US-09-997-601-219	Sequence 219, App
394	35	44.3	389	4	US-10-437-963-191059	Sequence 191059,	467	35	44.3	632	3	US-09-980-443-219	Sequence 219, App
395	35	44.3	394	3	US-09-833-245-1498	Sequence 1498, Ap	468	35	44.3	632	3	US-09-991-854-219	Sequence 219, App
396	35	44.3	395	4	US-10-108-260A-4617	Sequence 4617, Ap	469	35	44.3	632	3	US-09-997-628-219	Sequence 219, App
397	35	44.3	407	5	US-10-128-558-369	Sequence 369, App	470	35	44.3	632	3	US-09-997-683-219	Sequence 219, App
398	35	44.3	408	4	US-10-377-636-2	Sequence 21, Appl	471	35	44.3	632	3	US-09-989-729A-219	Sequence 219, App
399	35	44.3	412	3	US-09-854-731-21	Sequence 21, Appl	472	35	44.3	632	3	US-09-997-349-219	Sequence 219, App
400	35	44.3	414	4	US-10-425-114-40798	Sequence 40798, A	473	35	44.3	632	3	US-09-997-440-219	Sequence 219, App
401	35	44.3	419	3	US-09-726-643-50	Sequence 50, Appl	474	35	44.3	632	3	US-09-990-440-219	Sequence 219, App
402	35	44.3	419	4	US-10-042-141-50	Sequence 50, Appl	475	35	44.3	632	3	US-09-997-857-219	Sequence 219, App
403	35	44.3	419	5	US-10-918-272-50	Sequence 50, Appl	476	35	44.3	632	3	US-09-993-469-219	Sequence 219, App
404	35	44.3	422	5	US-10-739-930-7796	Sequence 7796, Ap	477	35	44.3	632	3	US-09-987-542-219	Sequence 219, App
405	35	44.3	439	4	US-10-108-260A-3726	Sequence 3726, Ap	478	35	44.3	632	3	US-09-993-748-219	Sequence 219, App
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408	35	44.3	450	4	US-10-425-114-55292	Sequence 55292, A	481	35	44.3	632	3	US-09-989-328-219	Sequence 219, App
409	35	44.3	468	4	US-10-467-535-3	Sequence 3, Appli	482	35	44.3	632	3	US-09-993-583-219	Sequence 219, App
410	35	44.3	471	4	US-10-424-599-266578	Sequence 266578,	483	35	44.3	632	3	US-09-941-992-219	Sequence 219, App
411	35	44.3	481	4	US-10-425-114-43080	Sequence 43080, A	484	35	44.3	632	3	US-09-992-521-219	Sequence 219, App
412	35	44.3	489	4	US-10-424-599-206716	Sequence 206716,	485	35	44.3	632	3	US-09-997-333-219	Sequence 219, App
413	35	44.3	506	5	US-10-343-903-17	Sequence 17, Appl	486	35	44.3	632	3	US-09-997-384-219	Sequence 219, App
414	35	44.3	542	4	US-10-425-114-68236	Sequence 68236, A	487	35	44.3	632	3	US-09-998-041-219	Sequence 219, App
415	35	44.3	542	4	US-10-425-115-360619	Sequence 360619,	488	35	44.3	632	3	US-09-997-585-219	Sequence 219, App
416	35	44.3	549	4	US-10-425-114-64633	Sequence 64633, A	489	35	44.3	632	3	US-09-989-862-219	Sequence 219, App
417	35	44.3	550	5	US-10-450-763-47076	Sequence 47076, A	490	35	44.3	632	3	US-09-989-829-219	Sequence 219, App
418	35	44.3	554	4	US-10-408-765A-2951	Sequence 2951, Ap	491	35	44.3	632	3	US-09-989-725-219	Sequence 219, App
419	35	44.3	562	4	US-10-369-493-10182	Sequence 10182, A	492	35	44.3	632	3	US-09-991-150-219	Sequence 219, App
420	35	44.3	563	4	US-10-369-493-975	Sequence 975, App	493	35	44.3	632	3	US-09-997-641-219	Sequence 219, App
421	35	44.3	571	4	US-10-369-493-39	Sequence 39, Appl	494	35	44.3	632	3	US-09-989-733-219	Sequence 219, App
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424	35	44.3	628	6	US-11-097-143-13773	Sequence 13773, A	497	35	44.3	632	4	US-10-052-586-166	Sequence 166, App
425	35	44.3	631	5	US-10-501-282-1256	Sequence 1256, Ap	498	35	44.3	632	4	US-10-063-547-40	Sequence 40, Appl
426	35	44.3	632	3	US-09-989-722-219	Sequence 219, App	499	35	44.3	632	4	US-10-063-551-40	Sequence 40, Appl
427	35	44.3	632	3	US-09-989-723-219	Sequence 219, App	500	35	44.3	632	4	US-10-174-590-166	Sequence 166, App
428	35	44.3	632	3	US-09-989-727-219	Sequence 219, App	501	35	44.3	632	4	US-10-176-758-166	Sequence 166, App
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442	35	44.3	632	3	US-09-991-181-219	Sequence 219, App	515	35	44.3	632	4	US-10-175-738-166	Sequence 166, App
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ALIGNMENTS

RESULT 1
US-10-517-510-4
; Sequence 4, Application US/10517510
; Publication No. US20050164201A1
; GENERAL INFORMATION:
; APPLICANT: Harvey, Diane Marie
; APPLICANT: Yang, Yi
; APPLICANT: Kohl, Nancy
; TITLE OF INVENTION: ISOLATED NUCLEIC ACID MOLECULE ENCODING
; TITLE OF INVENTION: A NOVEL CENTROMERE-ASSOCIATED MOTOR PROTEIN, AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: 21023P
; CURRENT APPLICATION NUMBER: US/10/517,510
; CURRENT FILING DATE: 2004-12-10
; PRIOR APPLICATION NUMBER: PCT/US03/18203
; PRIOR FILING DATE: 2003-06-09
; PRIOR APPLICATION NUMBER: 60/387,403
; PRIOR FILING DATE: 2002-06-10
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 355
; TYPE: PRT
; ORGANISM: Human
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Best Local Similarity 100.0%; Pred. No. 1.4e-05;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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; Sequence 2, Application US/10517510
; Publication No. US20050164201A1
; GENERAL INFORMATION:
; APPLICANT: Harvey, Diane Marie
; APPLICANT: Yang, Yi
; APPLICANT: Kohl, Nancy
; TITLE OF INVENTION: ISOLATED NUCLEIC ACID MOLECULE ENCODING
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: 21023P
; CURRENT APPLICATION NUMBER: US/10/517,510
; CURRENT FILING DATE: 2004-12-10
; PRIOR APPLICATION NUMBER: PCT/US03/18203
; PRIOR FILING DATE: 2003-06-09
; PRIOR APPLICATION NUMBER: 60/387,403
; PRIOR FILING DATE: 2002-06-10
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 355
; TYPE: PRT
; ORGANISM: Human
US-10-517-510-2
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Best Local Similarity 100.0%; Pred. No. 1.4e-05;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 3
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; Sequence 11, Application US/10828985A
; Publication No. US20050003402A1
; GENERAL INFORMATION:
; APPLICANT: Armour, Christopher D
; APPLICANT: Castle, John C
; APPLICANT: Garrett-Engle, Philip W
; APPLICANT: Kan, Zhengyan
; APPLICANT: Loerch, Patrick M
; APPLICANT: Tsinoremas, Nicholas F
; TITLE OF INVENTION: Novel Isoforms of Centromere Protein E (CENPE)
; FILE REFERENCE: RS0210Y
; CURRENT APPLICATION NUMBER: US/10/828,985A
; CURRENT FILING DATE: 2004-04-21
; PRIOR APPLICATION NUMBER: US 60/464,905
; PRIOR FILING DATE: 2003-04-23
; PRIOR APPLICATION NUMBER: US 60/510,701
; PRIOR FILING DATE: 2003-10-10
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn version 3.2
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US-10-828-985A-11
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Db 189 RHYGETKNQSRSS 203

RESULT 4
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; Publication No. US20050003402A1
; GENERAL INFORMATION:
; APPLICANT: Armour, Christopher D
; APPLICANT: Castle, John C
; APPLICANT: Garrett-Engle, Philip W
; APPLICANT: Kan, Zhengyan
; APPLICANT: Loerch, Patrick M
; APPLICANT: Tsinoremas, Nicholas F
; TITLE OF INVENTION: ISOLATED NUCLEIC ACID MOLECULE ENCODING
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: 21023P
; CURRENT APPLICATION NUMBER: US/10/517,510
; CURRENT FILING DATE: 2004-12-10
; PRIOR APPLICATION NUMBER: PCT/US03/18203
; PRIOR FILING DATE: 2003-06-09
; PRIOR APPLICATION NUMBER: 60/387,403
; PRIOR FILING DATE: 2002-06-10
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 496
; TYPE: PRT
; ORGANISM: Human
US-10-517-510-2
Query Match 100.0%; Score 79; DB 5; Length 496;
Best Local Similarity 100.0%; Pred. No. 2e-05;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RHYGETKNQSRSS 15
Db 189 RHYGETKNQSRSS 203
```


APPLICANT: Sakowicz, Roman
APPLICANT: Goldstein, Lawrence S.B.
APPLICANT: Cleveland, Don W.
APPLICANT: The Regents of the University of California
TITLE OF INVENTION: Plus End-Directed Microtubule Motor Required for
FILE REFERENCE: 18557C-000110US
CURRENT APPLICATION NUMBER: US/10/650,280
CURRENT FILING DATE: 2003-08-27
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US/09/150,867
PRIOR FILING DATE: EARLIER FILING DATE: 1998-09-10
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/058,645
PRIOR FILING DATE: EARLIER FILING DATE: 1997-09-11
NUMBER OF SEQ ID NOS: 11
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 1
LENGTH: 2954
TYPE: PRT
ORGANISM: Xenopus sp.
FEATURE:
OTHER INFORMATION: Xenopus centromere-associated protein-E (XCENP-E)
OTHER INFORMATION: member of the kinesin superfamily of microtubule
OTHER INFORMATION: motor proteins
FEATURE:
NAME/KEY: DOMAIN
LOCATION: (1)..(472)
OTHER INFORMATION: kinesin like motor domain
FEATURE:
NAME/KEY: DOMAIN
LOCATION: (473)..(2752)
OTHER INFORMATION: rod domain
FEATURE:
NAME/KEY: DOMAIN
LOCATION: (2753)..(2954)
OTHER INFORMATION: tail domain
US-10-650-280-1

Query Match 87.3%; Score 69; DB 5; Length 2954;
Best Local Similarity 86.7%; Pred. No. 0.0081;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 RHYGETKNQRRSRS 15
Db 187 RHYGETKNQRRSRS 201

RESULT 9
US-10-425-115-263022
Sequence 263022, Application US/10425115
Publication No. US20040214272A1
GENERAL INFORMATION:
APPLICANT: La Rosa, Thomas J.
APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
FILE REFERENCE: 38-21(53222)B
CURRENT APPLICATION NUMBER: US/10/425,115
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 369326
SEQ ID NO 263022
LENGTH: 668
TYPE: PRT
ORGANISM: Zea mays
FEATURE:
OTHER INFORMATION: Clone ID: MRT4577_171488C.1.pep
US-10-425-115-263022

Query Match 82.3%; Score 65; DB 4; Length 668;
Best Local Similarity 80.0%; Pred. No. 0.0086;
Matches 12; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 RHYGETKNQRRSRS 15
Db 195 RHFGETNMNRSSRS 209

RESULT 10
US-10-425-114-59725
Sequence 59725, Application US/10425114
Publication No. US20040034888A1
GENERAL INFORMATION:
APPLICANT: Liu, Jingdong
APPLICANT: Zhou, Yihua
APPLICANT: Kovalic, David K.
APPLICANT: Screen, Steven E
APPLICANT: Tabaska, Jack E
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
FILE REFERENCE: 38-21(53313)B
CURRENT APPLICATION NUMBER: US/10/425,114
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 73128
SEQ ID NO 59725
LENGTH: 694
TYPE: PRT
ORGANISM: Zea mays
FEATURE:
OTHER INFORMATION: Clone ID: LIB3912-011-C4_FLI.pep
US-10-425-114-59725

Query Match 82.3%; Score 65; DB 4; Length 694;
Best Local Similarity 80.0%; Pred. No. 0.0089;
Matches 12; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 RHYGETKNQRRSRS 15
Db 221 RHFGETNMNRSSRS 235

RESULT 11
US-10-437-963-116808
Sequence 116808, Application US/10437963
Publication No. US2004012343A1
GENERAL INFORMATION:
APPLICANT: La Rosa, Thomas J.
APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
APPLICANT: Wu, Wei
APPLICANT: Boukharov, Andrey A.
APPLICANT: Barbazuk, Brad
APPLICANT: Li, Ping
TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
FILE REFERENCE: 38-21(53221)B
CURRENT APPLICATION NUMBER: US/10/437,963
CURRENT FILING DATE: 2003-05-14
NUMBER OF SEQ ID NOS: 204966
SEQ ID NO 116808
LENGTH: 201
TYPE: PRT
ORGANISM: Oryza sativa
FEATURE:
OTHER INFORMATION: Clone ID: PAT_MRT4530_20274C.1.pep
US-10-437-963-116808

Query Match 79.7%; Score 63; DB 4; Length 201;
Best Local Similarity 80.0%; Pred. No. 0.0054;
Matches 12; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 RHYGETKNQRRSRS 15
Db 41 RHFGETNMNRSSRS 55

```
RESULT 12
US-11-097-143-13758
; Sequence 13758, Application US/11097143
; Publication No. US20050208558A1
; GENERAL INFORMATION:
; APPLICANT: Venter, J. Craig
; APPLICANT: et al.
; TITLE OF INVENTION: DETECTION KIT, SUCH AS NUCLEIC ACID
; TITLE OF INVENTION: ARRAYS, FOR DETECTING EXPRESSION OF 10,000 OR MORE
; TITLE OF INVENTION: DROSOPHILA GENES.
; FILE REFERENCE: CL000728
; CURRENT APPLICATION NUMBER: US/11/097,143
; CURRENT FILING DATE: 2005-04-04
; PRIOR APPLICATION NUMBER: 60/157,832
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: 60/160,191
; PRIOR FILING DATE: 1999-10-19
; PRIOR APPLICATION NUMBER: 60/161,932
; PRIOR FILING DATE: 1999-10-28
; PRIOR APPLICATION NUMBER: 60/164,769
; PRIOR FILING DATE: 1999-11-12
; PRIOR APPLICATION NUMBER: 60/173,383
; PRIOR FILING DATE: 1999-12-28
; PRIOR APPLICATION NUMBER: 60/175,693
; PRIOR FILING DATE: 2000-01-12
; PRIOR APPLICATION NUMBER: 60/184,831
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: 60/191,637
; PRIOR FILING DATE: 2000-03-23
; NUMBER OF SEQ ID NOS: 43008
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13758
; LENGTH: 2013
; TYPE: PRT
; ORGANISM: DROSOPHILA
US-11-097-143-13758

Query Match 67.1%; Score 53; DB 6; Length 2013;
Best Local Similarity 73.3%; Pred. No. 3.8;
Matches 11; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 RHYGETKNQRRSSRS 15
| | | | | | | | | | | | | | |
DB 183 RTVGETNNVSSRS 197

RESULT 13
US-09-864-408A-1218
; Sequence 1218, Application US/09864408A
; Publication No. US20040009474A1
; GENERAL INFORMATION:
; APPLICANT: Leach, Martin D.
; APPLICANT: Shimkete, Richard A.
; TITLE OF INVENTION: No. US20040009474A1el Human Polynucleotides and Polypeptides Encod
; FILE REFERENCE: 21402-012
; CURRENT APPLICATION NUMBER: US/09/864,408A
; CURRENT FILING DATE: 2001-05-24
; PRIOR APPLICATION NUMBER: 60/206,690
; PRIOR FILING DATE: 2000-03-24
; NUMBER OF SEQ ID NOS: 9068
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1218
; LENGTH: 154
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)-(1)
; OTHER INFORMATION: Wherein Xaa may be any naturally occurring amino acid
US-09-864-408A-1218
```

```
Query Match 65.8%; Score 52; DB 3; Length 154;
Best Local Similarity 66.7%; Pred. No. 0.37;
Matches 10; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 RHYGETKNQRRSSRS 15
| | | | | | | | | | | | | | |
DB 29 RHTGTTQWNEHSSRS 43

RESULT 14
US-10-437-963-176714
; Sequence 176714, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 176714
; LENGTH: 1382
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_74437C.1.pep
US-10-437-963-176714

Query Match 65.8%; Score 52; DB 4; Length 1382;
Best Local Similarity 73.3%; Pred. No. 3.9;
Matches 11; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 RHYGETKNQRRSSRS 15
| | | | | | | | | | | | | | |
DB 180 RHIGETNNVYSSRS 194

RESULT 15
US-10-287-226-142
; Sequence 142, Application US/10287226
; Publication No. US20040086875A1
; GENERAL INFORMATION:
; APPLICANT: Agee, Michele L.,
; APPLICANT: Alsobrook, John P.,
; APPLICANT: Berghs, Constance,
; APPLICANT: Boldog, Renence,
; APPLICANT: Burgess, Catherine E.,
; APPLICANT: Chant, John S.,
; APPLICANT: Chaudhuri, Amitabha,
; APPLICANT: DiPippo, Vincent A.,
; APPLICANT: Edinger, Shlomit R.,
; APPLICANT: Eisen, Andrew,
; APPLICANT: Ellerman, Karen,
; APPLICANT: Gangolli, Esha A.,
; APPLICANT: Gorman, Linda,
; APPLICANT: Gerlach, Valerie,
; APPLICANT: Ji, Weizhen,
; APPLICANT: Kekuda, Ramesh,
; APPLICANT: Khrantsov, Nikolai,
; APPLICANT: Li, Li,
; APPLICANT: Malyankar, Uriel M.,
; APPLICANT: MacDougall, John R.,
; APPLICANT: Mezes, Peter S.,
; APPLICANT: Miller, Charles E.,
; APPLICANT: Millet, Isabelle,
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/ APPLICANT: Ooi, Chean Eng,
/ APPLICANT: Ort, Tatiana,
/ APPLICANT: Padigaru, Muralidhara,
/ APPLICANT: Patturajan, Meera,
/ APPLICANT: Rastelli, Luca,
/ APPLICANT: Rieger, Daniel K.,
/ APPLICANT: Rothenberg, Mark B.,
/ APPLICANT: Shenoy, Suresh G.,
/ APPLICANT: Spaderina, Steven K.,
/ APPLICANT: Spytek, Kimberley A.,
/ APPLICANT: Taupier, Jr., Raymond J.,
/ APPLICANT: Vernet, Corine A.M.,
/ APPLICANT: Zerhusen, Bryan D.,
/ APPLICANT: Zhong, Mei
/ TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME
/ FILE REFERENCE: 21402-480C
/ CURRENT APPLICATION NUMBER: US/10/287,226
/ CURRENT FILING DATE: 2002-11-04
/ PRIOR APPLICATION NUMBER: 60/334,421
/ PRIOR FILING DATE: 2001-11-30
/ PRIOR APPLICATION NUMBER: 60/354,392
/ PRIOR FILING DATE: 2002-02-04
/ PRIOR APPLICATION NUMBER: 60/360,148
/ PRIOR FILING DATE: 2002-02-27
/ PRIOR APPLICATION NUMBER: 60/364,000
/ PRIOR FILING DATE: 2002-03-13
/ PRIOR APPLICATION NUMBER: 60/404,821
/ PRIOR FILING DATE: 2002-08-20
/ PRIOR APPLICATION NUMBER: 60/334,526
/ PRIOR FILING DATE: 2001-11-30
/ PRIOR APPLICATION NUMBER: 60/354,409
/ PRIOR FILING DATE: 2002-02-04
/ PRIOR APPLICATION NUMBER: 60/364,227
/ PRIOR FILING DATE: 2002-03-13
/ PRIOR APPLICATION NUMBER: 60/334,027
/ PRIOR FILING DATE: 2001-11-28
/ PRIOR APPLICATION NUMBER: 60/331,641
/ PRIOR FILING DATE: 2001-11-20
/ Remaining Prior Application data removed - See File Wrapper or PALM.
/ NUMBER OF SEQ ID NOS: 673
/ SOFTWARE: CurSeqList version 0.1
/ SEQ ID NO 142
/ LENGTH: 1401
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-10-287-226-142

Query Match 65.8%; Score 52; DB 4; Length 1401;
Best Local Similarity 66.7%; Pred. No. 3.9;
Matches 10; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 RHYGETKNQRRSRS 15
||| ||| ||| ||| |||
Db 193 RHTGTQNEHSRS 207

RESULT 16
US-11-097-143-9828
/ Sequence 9828, Application US/11097143
/ Publication No. US20050208558A1
/ GENERAL INFORMATION:
/ APPLICANT: Venter, J. Craig
/ APPLICANT: et al.
/ TITLE OF INVENTION: DETECTION KIT, SUCH AS NUCLEIC ACID
/ TITLE OF INVENTION: ARRAYS, FOR DETECTING EXPRESSION OF 10,000 OR MORE
/ TITLE OF INVENTION: DROSOPHILA GENES.
/ FILE REFERENCE: CL000728
/ CURRENT APPLICATION NUMBER: US/11/097,143
/ CURRENT FILING DATE: 2005-04-04
/ PRIOR APPLICATION NUMBER: 60/157,832
/ PRIOR FILING DATE: 1999-10-05
/ PRIOR APPLICATION NUMBER: 60/160,191
/ PRIOR FILING DATE: 1999-10-19
/
```

```
/ PRIOR APPLICATION NUMBER: 60/161,932
/ PRIOR FILING DATE: 1999-10-28
/ PRIOR APPLICATION NUMBER: 60/164,769
/ PRIOR FILING DATE: 1999-11-12
/ PRIOR APPLICATION NUMBER: 60/173,383
/ PRIOR FILING DATE: 1999-12-28
/ PRIOR APPLICATION NUMBER: 60/175,693
/ PRIOR FILING DATE: 2000-01-12
/ PRIOR APPLICATION NUMBER: 60/184,831
/ PRIOR FILING DATE: 2000-02-24
/ PRIOR APPLICATION NUMBER: 60/191,637
/ PRIOR FILING DATE: 2000-03-23
/ NUMBER OF SEQ ID NOS: 43008
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 9828
/ LENGTH: 1931
/ TYPE: PRT
/ ORGANISM: DROSOPHILA
US-11-097-143-9828

Query Match 65.8%; Score 52; DB 6; Length 1931;
Best Local Similarity 73.3%; Pred. No. 5.5;
Matches 11; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 RHYGETKNQRRSRS 15
||| ||| ||| ||| |||
Db 183 RVGGETNNERSRS 197

RESULT 17
US-10-425-115-245875
/ Sequence 245875, Application US/10425115
/ Publication No. US20040214272A1
/ GENERAL INFORMATION:
/ APPLICANT: La Rosa, Thomas J.
/ APPLICANT: Kowalic, David K.
/ APPLICANT: Zhou, Yihua
/ APPLICANT: Cao, Yongwei
/ TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
/ TITLE OF INVENTION: Plants
/ FILE REFERENCE: 38-21(53222)B
/ CURRENT APPLICATION NUMBER: US/10/425,115
/ CURRENT FILING DATE: 2003-04-28
/ NUMBER OF SEQ ID NOS: 369326
/ SEQ ID NO 245875
/ LENGTH: 197
/ TYPE: PRT
/ ORGANISM: Zea mays
/ FEATURE:
/ OTHER INFORMATION: Clone ID: MRT4577_155820C.1.pep
US-10-425-115-245875

Query Match 64.6%; Score 51; DB 4; Length 197;
Best Local Similarity 73.3%; Pred. No. 0.73;
Matches 11; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 RHYGETKNQRRSRS 15
||| ||| ||| ||| |||
Db 167 RHIGETDNNLYSRS 181

RESULT 18
US-11-097-143-22341
/ Sequence 22341, Application US/11097143
/ Publication No. US20050208558A1
/ GENERAL INFORMATION:
/ APPLICANT: Venter, J. Craig
/ APPLICANT: et al.
/ TITLE OF INVENTION: DETECTION KIT, SUCH AS NUCLEIC ACID
/ TITLE OF INVENTION: ARRAYS, FOR DETECTING EXPRESSION OF 10,000 OR MORE
/ TITLE OF INVENTION: DROSOPHILA GENES.
/ FILE REFERENCE: CL000728
/ CURRENT APPLICATION NUMBER: US/11/097,143
/
```

```

; CURRENT FILING DATE: 2005-04-04
; PRIOR APPLICATION NUMBER: 60/157,832
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: 60/160,191
; PRIOR FILING DATE: 1999-10-19
; PRIOR APPLICATION NUMBER: 60/161,932
; PRIOR FILING DATE: 1999-10-28
; PRIOR APPLICATION NUMBER: 60/164,769
; PRIOR FILING DATE: 1999-11-12
; PRIOR APPLICATION NUMBER: 60/173,383
; PRIOR FILING DATE: 1999-12-28
; PRIOR APPLICATION NUMBER: 60/175,693
; PRIOR FILING DATE: 2000-01-12
; PRIOR APPLICATION NUMBER: 60/184,831
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: 60/191,637
; PRIOR FILING DATE: 2000-03-23
; NUMBER OF SEQ ID NOS: 43008
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 22341
; LENGTH: 677
; TYPE: PRT
; ORGANISM: DROSOPHILA
US-11-097-143-22341

```

```

Query Match      63.3%; Score 50; DB 6; Length 677;
Best Local Similarity 73.3%; Pred. NO. 4.1;
Matches 11; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy      1 RHYGETKNQNRSSRS 15
        | | | | | | | |
Db      213 RAVGATKNQNRSSRS 227

```

```

RESULT 19
US-10-425-115-210540
; Sequence 210540, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 210540
; LENGTH: 259
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_123610C.1.pep
; US-10-425-115-210540

```

```

Query Match      62.0%; Score 49; DB 4; Length 259;
Best local similarity 66.7%; Pred. No. 2.2;
Matches 10; Conservative 1; Mismatches 4; Indels 0; Gaps 0;
Qy      1 RHYGETGNQRSSRS 15
Db      167 RQIGETSNNEASSRS 181

```

RESULT 20
US-10-797-893-6
; Sequence 6, Application US/10797893
; Publication No. US20040142397A1
; GENERAL INFORMATION:
; APPLICANT: Beraud, Christophe
; TITLE OF INVENTION: Novel motor proteins and methods for

```

, TITLE OF INVENTION: their use
, FILE REFERENCE: 1044
, CURRENT APPLICATION NUMBER: US/10/797,893
, CURRENT FILING DATE: 2004-03-09
, PRIOR APPLICATION NUMBER: US/09/724,224
, PRIOR FILING DATE: 2000-11-28
, PRIOR APPLICATION NUMBER: 09/597,292
, PRIOR FILING DATE: 2000-06-20
, NUMBER OF SEQ ID NOS: 8
, SOFTWARE: FastSeq for Windows Version 4.0
, SEQ ID NO 6
, LENGTH: 346
, TYPE: prt
, ORGANISM: Human
, US-10-797-893-6

```

Query Match 62.0%; Score 49; DB 4; Length 346;
Best Local Similarity 66.7%; Pred. No. 3;
Matches 10: Conservative 2; Mismatches 3; Indels 0; Gaps 0;

```

RESULT 21
US-10-797-893-2
; Sequence 2, Application US/10797893
; Publication No. US20040142397A1
; GENERAL INFORMATION:
; APPLICANT: Beraud, Christophe
; TITLE OF INVENTION: Novel motor proteins and methods for
; FILE OF INVENTION: their use
; FILE REFERENCE: 1044
; CURRENT APPLICATION NUMBER: US/10/797,893
; CURRENT FILING DATE: 2004-03-09
; PRIOR APPLICATION NUMBER: US/09/724,224
; PRIOR FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: 09/597,292
; PRIOR FILING DATE: 2000-06-20
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: Fast-SEQ for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 370
; TYPE: PRT
; ORGANISM: Human
US-10-797-893-2

```

```

Query Match      62.0%; Score 49; DB 4; Length 370;
Best Local Similarity 66.7%; Pred. No. 3.3;
Matches 10; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY      1 RHYGETKQNRSSRS 15
Db      232 RTVGATLNQNRSSRS 246

```

```

RESULT 22
US-09-925-300-1228
; Sequence 1228, Application US/09925300
; Patent No. US20020151681A1
;
; GENERAL INFORMATION:
;   APPLICANT: Craig Rosen,
;   APPLICANT: Steve Ruben
;   TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
;   FILE REFERENCE: PA101
;   CURRENT APPLICATION NUMBER: US/09/925.300
;   CURRENT FILING DATE: 2001-08-10
;   PRIOR APPLICATION NUMBER: PCT/US00/005988
;   PRIOR FILING DATE: 2000-03-08
;   PRIOR APPLICATION NUMBER: 60/124,270
;   PRIOR FILING DATE: 1999-03-12
;   NUMBER OF SEQ ID NOS: 1890

```

```
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1228
; LENGTH: 460
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (75)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (147)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (435)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-09-925-300-1228

Query Match          62.0%; Score 49; DB 3; Length 460;
Best Local Similarity 66.7%; Pred. No. 4.1;
Matches 10; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 RHYGETKNQSRSS 15
Db 210 RTVGATRLNQSRSS 224

RESULT 23
US-10-797-893-8
; Sequence 8, Application US/10797893
; Publication No. US20040142397A1
; GENERAL INFORMATION:
; APPLICANT: Beraud, Christophe
; TITLE OF INVENTION: Novel motor proteins and methods for
; FILE REFERENCE: 1044
; CURRENT APPLICATION NUMBER: US/10/797,893
; PRIOR FILING DATE: 2004-03-09
; PRIOR APPLICATION NUMBER: US/09/724,224
; PRIOR FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: 09/597,292
; PRIOR FILING DATE: 2000-06-20
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 487
; TYPE: PRT
; ORGANISM: Human
US-10-797-893-8

Query Match          62.0%; Score 49; DB 4; Length 487;
Best Local Similarity 66.7%; Pred. No. 4.4;
Matches 10; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 RHYGETKNQSRSS 15
Db 208 RTVGATRLNQSRSS 222

RESULT 24
US-10-334-143-80
; Sequence 80, Application US/10334143
; Publication No. US20040009549A1
; GENERAL INFORMATION:
; APPLICANT: GRIGORIEV, IGOR VYACHESLAVOVICH
; APPLICANT: SUDARSANAM, SVACHA
; TITLE OF INVENTION: METHOD FOR DETECTING REMOTE HOMOLOGUES AND NOVEL
; TITLE OF INVENTION: KINASES IDENTIFIED WITH THE METHOD
; FILE REFERENCE: 038602/1543
; CURRENT APPLICATION NUMBER: US/10/334,143
; CURRENT FILING DATE: 2002-12-31
; PRIOR APPLICATION NUMBER: 60/343,169
; PRIOR FILING DATE: 2001-12-31
; NUMBER OF SEQ ID NOS: 207
```

```
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 80
; LENGTH: 490
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-334-143-80

Query Match          62.0%; Score 49; DB 4; Length 490;
Best Local Similarity 66.7%; Pred. No. 4.4;
Matches 10; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 RHYGETKNQSRSS 15
Db 240 RTVGATRLNQSRSS 254

RESULT 25
US-10-797-893-4
; Sequence 4, Application US/10797893
; Publication No. US20040142397A1
; GENERAL INFORMATION:
; APPLICANT: Beraud, Christophe
; TITLE OF INVENTION: Novel motor proteins and methods for
; FILE REFERENCE: 1044
; CURRENT APPLICATION NUMBER: US/10/797,893
; PRIOR FILING DATE: 2004-03-09
; PRIOR APPLICATION NUMBER: US/09/724,224
; PRIOR FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: 09/597,292
; PRIOR FILING DATE: 2000-06-20
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 512
; TYPE: PRT
; ORGANISM: Human
US-10-797-893-4

Query Match          62.0%; Score 49; DB 4; Length 512;
Best Local Similarity 66.7%; Pred. No. 4.6;
Matches 10; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 RHYGETKNQSRSS 15
Db 233 RTVGATRLNQSRSS 247

RESULT 26
US-10-733-878-425
; Sequence 425, Application US/10733878
; Publication No. US20040224408A1
; GENERAL INFORMATION:
; APPLICANT: Jean-Philippe Girard
; APPLICANT: Francois Amalric
; APPLICANT: Myriam Roussigne
; APPLICANT: Thomas Clouaire
; TITLE OF INVENTION: THAP PROTEINS AS NUCLEAR RECEPTORS FOR
; TITLE OF INVENTION: CHEMOKINES AND ROLES IN TRANSCRIPTIONAL REGULATION, CELL
; TITLE OF INVENTION: PROLIFERATION AND CELL DIFFERENTIATION
; FILE REFERENCE: BIOBANK.012A
; CURRENT APPLICATION NUMBER: US/10/733,878
; CURRENT FILING DATE: 2003-12-10
; PRIOR APPLICATION NUMBER: 60/432699
; PRIOR FILING DATE: 2002-12-10
; PRIOR APPLICATION NUMBER: 60/485027
; PRIOR FILING DATE: 2003-07-03
; NUMBER OF SEQ ID NOS: 535
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 425
; LENGTH: 665
; TYPE: PRT
; ORGANISM: Homo sapiens
```


US-10-733-878-425

Query Match 62.0%; Score 49; DB 5; Length 665;
Best Local Similarity 66.7%; Pred. No. 6.1;
Matches 10; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 RHYGETKMNQSSRS 15
|||:|||||
Db 232 RTVGATRLNQSSRS 246

RESULT 27

US-09-874-923-53

; Sequence 53, Application US/09874923
; Patent No. US20020081320A1
; GENERAL INFORMATION:
; APPLICANT: Reed, Steven G.
; APPLICANT: Campos-Neto, Antonio
; APPLICANT: Webb, John R.
; APPLICANT: Dillon, Davin C.
; APPLICANT: Skeiky, Yaseir A.W.
; APPLICANT: Bhatia, Ajay
; APPLICANT: Coler, Rhea
; APPLICANT: Probst, Peter
; APPLICANT: Brannon, Mark
; TITLE OF INVENTION: LEISHMANIA ANTIGENS FOR USE IN THE
; FILE REFERENCE: 210121.420C8
; CURRENT APPLICATION NUMBER: US/09/874,923
; CURRENT FILING DATE: 2001-06-04
; NUMBER OF SEQ ID NOS: 122
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 53
; LENGTH: 324
; TYPE: PRT
; ORGANISM: Leishmania chagasi
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (1)...(324)
; OTHER INFORMATION: Xaa = Any Amino Acid
US-09-874-923-53

Query Match 60.8%; Score 48; DB 3; Length 324;
Best Local Similarity 66.7%; Pred. No. 4.3;
Matches 10; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 RHYGETKMNQSSRS 15
|||:|||||
Db 234 RHTAATKFNDRSSRS 248

RESULT 28

US-09-991-496-53

; Sequence 53, Application US/09991496
; Patent No. US20020169285A1
; GENERAL INFORMATION:
; APPLICANT: Reed, Steven G.
; APPLICANT: Campos-Neto, Antonio
; APPLICANT: Webb, John R.
; APPLICANT: Dillon, Davin C.
; APPLICANT: Skeiky, Yaseir A.W.
; APPLICANT: Bhatia, Ajay
; APPLICANT: Coler, Rhea
; APPLICANT: Probst, Peter
; APPLICANT: Brannon, Mark
; TITLE OF INVENTION: LEISHMANIA ANTIGENS FOR USE IN THE
; FILE REFERENCE: 210121.420C9
; CURRENT APPLICATION NUMBER: US/09/991,496
; CURRENT FILING DATE: 2001-11-20
; NUMBER OF SEQ ID NOS: 137
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 53

; LENGTH: 324

; TYPE: PRT

; ORGANISM: Leishmania chagasi

; FEATURE:

; NAME/KEY: VARIANT

; LOCATION: 79, 96

; OTHER INFORMATION: Xaa = Any Amino Acid

US-09-991-496-53

Query Match

Best Local Similarity 60.8%; Score 48; DB 3; Length 324;

Matches 10; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 RHYGETKMNQSSRS 15

|||:|||||

Db 234 RHTAATKFNDRSSRS 248

RESULT 29

US-10-437-963-114373

; Sequence 114373, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated with
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 114373
; LENGTH: 420
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_18070C.1.pep
US-10-437-963-114373

Query Match 60.8%; Score 48; DB 4; Length 420;
Best Local Similarity 66.7%; Pred. No. 5.6;
Matches 10; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 RHYGETKMNQSSRS 15

|||:|||||

Db 197 RQIGETAMNEASSRS 211

RESULT 30

US-10-437-963-114370

; Sequence 114370, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated with
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966

```
; SEQ ID NO 114370
; LENGTH: 821
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_18069C.1.pep
US-10-437-963-114370

Query Match          60.8%; Score 48; DB 4; Length 821;
Best Local Similarity 66.7%; Pred. No. 11;
Matches 10; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 RHYGETKNQRRSSRS 15
    |||||:||||
Db 167 ROIGETANNEASSRS 181

RESULT 31
US-10-437-963-163527
; Sequence 163527, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 163527
; LENGTH: 906
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_62515C.1.pep
US-10-437-963-163527

Query Match          60.8%; Score 48; DB 4; Length 906;
Best Local Similarity 66.7%; Pred. No. 13;
Matches 10; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 RHYGETKNQRRSSRS 15
    |||||:||||
Db 206 RHAANTKMTSSRS 220

RESULT 32
US-09-826-734-144
; Sequence 144, Application US/09826734
; Publication No. US20030017457A1
; GENERAL INFORMATION:
; APPLICANT: Fernandes, Elma R.
; APPLICANT: Vernet, Corine A.M.
; APPLICANT: Mishra, Vishnu S.
; APPLICANT: Leach, Martin D.
; APPLICANT: Shinkete, Richard A.
; APPLICANT: Zerhusen, Bryan D.
; APPLICANT: Kekuda, Ramesha
; TITLE OF INVENTION: Novel Polynucleotides and Polypeptides Encoded Thereby
; FILE REFERENCE: 15966-754
; CURRENT APPLICATION NUMBER: US/09/826,734
; CURRENT FILING DATE: 2001-04-05
; PRIOR APPLICATION NUMBER: 60/195,576
; PRIOR FILING DATE: 2000-04-06
; NUMBER OF SEQ ID NOS: 270
; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 114370
; LENGTH: 821
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_18069C.1.pep
US-10-437-963-114370

Query Match          60.8%; Score 48; DB 4; Length 821;
Best Local Similarity 66.7%; Pred. No. 11;
Matches 10; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 RHYGETKNQRRSSRS 15
    |||||:||||
Db 167 ROIGETANNEASSRS 181

RESULT 31
US-10-437-963-163527
; Sequence 163527, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 163527
; LENGTH: 906
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_62515C.1.pep
US-10-437-963-163527

Query Match          60.8%; Score 48; DB 4; Length 906;
Best Local Similarity 66.7%; Pred. No. 13;
Matches 10; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 RHYGETKNQRRSSRS 15
    |||||:||||
Db 206 RHAANTKMTSSRS 220

RESULT 32
US-09-826-734-144
; Sequence 144, Application US/09826734
; Publication No. US20030017457A1
; GENERAL INFORMATION:
; APPLICANT: Fernandes, Elma R.
; APPLICANT: Vernet, Corine A.M.
; APPLICANT: Mishra, Vishnu S.
; APPLICANT: Leach, Martin D.
; APPLICANT: Shinkete, Richard A.
; APPLICANT: Zerhusen, Bryan D.
; APPLICANT: Kekuda, Ramesha
; TITLE OF INVENTION: Novel Polynucleotides and Polypeptides Encoded Thereby
; FILE REFERENCE: 15966-754
; CURRENT APPLICATION NUMBER: US/09/826,734
; CURRENT FILING DATE: 2001-04-05
; PRIOR APPLICATION NUMBER: 60/195,576
; PRIOR FILING DATE: 2000-04-06
; NUMBER OF SEQ ID NOS: 270
; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 144
; LENGTH: 54
; TYPE: PRT
; ORGANISM: homo sapiens
; OTHER INFORMATION:
US-09-826-734-144

Query Match          59.5%; Score 47; DB 3; Length 54;
Best Local Similarity 64.3%; Pred. No. 0.95;
Matches 9; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 2 HYGETKNQRRSSRS 15
    |||||:||||
Db 1 HTGTTQMNHSRS 14

RESULT 33
US-10-424-599-152360
; Sequence 152360, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 152360
; LENGTH: 75
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(75)
; OTHER INFORMATION: unsure at all Xaa locations
; OTHER INFORMATION: Clone ID: PAT_MRT3847_108604C.1.pep
US-10-424-599-152360

Query Match          59.5%; Score 47; DB 4; Length 75;
Best Local Similarity 60.0%; Pred. No. 1.4;
Matches 9; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 1 RHYGETKNQRRSSRS 15
    |||||:||||
Db 2 RSVGKTQNEQSSRS 16

RESULT 34
US-10-425-115-201216
; Sequence 201216, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 201216
; LENGTH: 78
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_115095C.1.pep
US-10-425-115-201216
```

Query Match 59.5%; Score 47; DB 4; Length 78;
Best Local Similarity 64.3%; Pred. No. 1.4;
Matches 9; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 2 HYGETKNQRRSSRS 15
| | | | | : | | | |
DB 32 HVGETKQNRLPKS 45

RESULT 35
US-10-424-599-156142
; Sequence 156142, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 156142
; LENGTH: 247
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_112017C.1.pep
US-10-424-599-156142

Query Match 59.5%; Score 47; DB 4; Length 247;
Best Local Similarity 60.0%; Pred. No. 4.8;
Matches 9; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1 RHYGETKNQRRSSRS 15
| | | | | : | | | |
DB 206 RQVGETYLNKRSRS 220

RESULT 36
US-10-424-599-274019
; Sequence 274019, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 274019
; LENGTH: 272
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)...(272)
; OTHER INFORMATION: unsure at all Xaa locations
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_8945C.1.pep
US-10-424-599-274019

Query Match 59.5%; Score 47; DB 4; Length 272;
Best Local Similarity 60.0%; Pred. No. 5.3;
Matches 9; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 1 RHYGETKNQRRSSRS 15
| | | | | : | | | |
DB 116 RSVGKTQNEQSSRS 130

RESULT 37
US-10-425-114-59085
; Sequence 59085, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E
; APPLICANT: Tabaska, Jack E
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 59085
; LENGTH: 458
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: 700048432_FLI.pep
US-10-425-114-59085

Query Match 59.5%; Score 47; DB 4; Length 458;
Best Local Similarity 60.0%; Pred. No. 9.3;
Matches 9; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 1 RHYGETKNQRRSSRS 15
| | | | | : | | | |
DB 314 RSVGKTQNEQSSRS 328

RESULT 38
US-10-369-493-5967
; Sequence 5967, Application US/10369493
; Publication No. US20030233675A1
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Goldman, Barty S.
; APPLICANT: Chen, Xianfeng
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
; FILE REFERENCE: 38-10(52052)B
; CURRENT APPLICATION NUMBER: US/10/369,493
; CURRENT FILING DATE: 2003-02-28
; PRIOR APPLICATION NUMBER: US 60/360,039
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 5967
; LENGTH: 670
; TYPE: PRT
; ORGANISM: Caenorhabditis elegans
US-10-369-493-5967

Query Match 59.5%; Score 47; DB 4; Length 670;
Best Local Similarity 66.7%; Pred. No. 14;
Matches 10; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 RHYGETKNQRRSSRS 15
| | | | | : | | | |
DB 188 RHVGATLANKDSSRS 202

RESULT 39

US-10-425-115-200354
; Sequence 200354, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 200354
; LENGTH: 789
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(789)
; OTHER INFORMATION: unsure at all Xaa locations
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_11430C.1.pap
US-10-425-115-200354

Query Match 59.5%; Score 47; DB 4; Length 789;
Best Local Similarity 60.0%; Pred. No. 17;
Matches 9; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 1 RHYGETKNQSSRS 15
| | | | |
| | | | |
Db 633 RSVGKTQNEQSSRS 647

RESULT 40
US-10-437-963-173873
; Sequence 173873, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 173873
; LENGTH: 762
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_7186C.1.pap
US-10-437-963-173873

Query Match 58.2%; Score 46; DB 4; Length 762;
Best Local Similarity 60.0%; Pred. No. 24;
Matches 9; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1 RHYGETKNQSSRS 15
| | | | |
| | | | |
Db 607 RSVGKTQNEQSSRS 621

RESULT 41
US-10-437-963-173884

; Sequence 173884, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 173884
; LENGTH: 788
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_7187C.1.pap
US-10-437-963-173884

Query Match 58.2%; Score 46; DB 4; Length 788;
Best Local Similarity 60.0%; Pred. No. 25;
Matches 9; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1 RHYGETKNQSSRS 15
| | | | |
| | | | |
Db 632 RSVGKTQNEQSSRS 646

RESULT 42
US-10-473-276-1
; Sequence 1, Application US/10473276
; Publication No. US20040158893A1
; GENERAL INFORMATION:
; APPLICANT: Dickinson, Hugh
; APPLICANT: Spielman, Melissa
; APPLICANT: Scott, Roderick
; TITLE OF INVENTION: FINAL SEGREGATION OF MALE MEIOTIC PRODUCTS IN PLANTS
; FILE REFERENCE: 046658/269934
; CURRENT APPLICATION NUMBER: US/10/473,276
; CURRENT FILING DATE: 2003-09-30
; PRIOR APPLICATION NUMBER: PCT/GB02/01466
; PRIOR FILING DATE: 2002-03-28
; PRIOR APPLICATION NUMBER: GB 0108050.6
; PRIOR FILING DATE: 2001-03-30
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 932
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
US-10-473-276-1

Query Match 58.2%; Score 46; DB 4; Length 932;
Best Local Similarity 60.0%; Pred. No. 30;
Matches 9; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 RHYGETKNQSSRS 15
| | | | |
| | | | |
Db 207 RQVGETALNDKSSRS 221

RESULT 43
US-10-437-963-113879
; Sequence 113879, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.

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; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 113879
; LENGTH: 114
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_17625C.1.pep
US-10-437-963-113879

Query Match          57.0%; Score 45; DB 4; Length 114;
Best Local Similarity 60.0%; Pred. No. 4.8;
Matches 9; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1 RHYGETKNQRSRS 15
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Db 68 RRTGETFLNEKSSRS 82

RESULT 44
US-10-767-701-36255
; Sequence 36255, Application US/10767701
; Publication No. US20040172684A1
; GENERAL INFORMATION:
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53535)B
; CURRENT APPLICATION NUMBER: US/10/767,701
; CURRENT FILING DATE: 2004-01-29
; NUMBER OF SEQ ID NOS: 63128
; SEQ ID NO 36255
; LENGTH: 252
; TYPE: PRT
; ORGANISM: Sorghum bicolor
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(252)
; OTHER INFORMATION: unsure at all Xaa locations
; FEATURE:
; OTHER INFORMATION: Clone ID: SORBI-28MAY03-C8566_1.pep
US-10-767-701-36255

Query Match          57.0%; Score 45; DB 4; Length 252;
Best Local Similarity 60.0%; Pred. No. 11;
Matches 9; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 RHYGETKNQRSRS 15
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Db 180 RSVGRTQMNESRS 194

RESULT 45
US-10-424-599-174384
; Sequence 174384, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
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; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 174384
; LENGTH: 312
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
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US-10-424-599-174384

Query Match          57.0%; Score 45; DB 4; Length 312;
Best Local Similarity 60.0%; Pred. No. 14;
Matches 9; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 RHYGETKNQRSRS 15
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Db 103 RQIGETALNEASRS 117

RESULT 46
US-10-425-114-45648
; Sequence 45648, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E
; APPLICANT: Tabaska, Jack E
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53131)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 45648
; LENGTH: 328
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: 700282006_FLI.pep
US-10-425-114-45648

Query Match          57.0%; Score 45; DB 4; Length 328;
Best Local Similarity 60.0%; Pred. No. 15;
Matches 9; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 RHYGETKNQRSRS 15
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Db 178 RSVGRTQMNESRS 192

RESULT 47
US-10-425-115-243578
; Sequence 243578, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
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; SEQ ID NO 243578
; LENGTH: 413
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_153726C.1.pep
US-10-425-115-243578

Query Match      57.0%; Score 45; DB 4; Length 413;
Best Local Similarity 60.0%; Pred. No. 19;
Matches 9; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 RHYGETKNQRRSRS 15
Db 263 RSVGRQTQMESSRS 277

RESULT 48
US-10-437-963-196324
; Sequence 196324, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 196324
; LENGTH: 515
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_92186C.1.pep
US-10-437-963-196324

Query Match      57.0%; Score 45; DB 4; Length 515;
Best Local Similarity 60.0%; Pred. No. 24;
Matches 9; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 RHYGETKNQRRSRS 15
Db 363 RSVGRQTQMESSRS 377

RESULT 49
US-10-425-115-242676
; Sequence 242676, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 242676
; LENGTH: 788
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
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; OTHER INFORMATION: Clone ID: MRT4577_152904C.1.pep
US-10-425-115-242676

Query Match      57.0%; Score 45; DB 4; Length 788;
Best Local Similarity 60.0%; Pred. No. 38;
Matches 9; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1 RHYGETKNQRRSRS 15
Db 122 RRTGETFLNEKSSRS 136

RESULT 50
US-10-080-608A-17
; Sequence 17, Application US/10080608A
; Publication No. US20030198956A1
; GENERAL INFORMATION:
; APPLICANT: Makowski, Lee
; APPLICANT: Hyman, Paul
; APPLICANT: Williams, Mark
; TITLE OF INVENTION: STAGED ASSEMBLY OF NANOSTRUCTURES
; FILE REFERENCE: 8471-010-999
; CURRENT APPLICATION NUMBER: US/10/080,608A
; CURRENT FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 180
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 17
; LENGTH: 956
; TYPE: PRT
; ORGANISM: Mus musculus
; OTHER INFORMATION:
US-10-080-608A-17

Query Match      57.0%; Score 45; DB 4; Length 956;
Best Local Similarity 60.0%; Pred. No. 46;
Matches 9; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 1 RHYGETKNQRRSRS 15
Db 191 RHVAVTNNNEHSSRS 205

Search completed: April 21, 2006, 13:56:58
Job time : 180 secs
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GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: April 21, 2006, 13:54:16 ; Search time 26 seconds
(without alignment)
25.386 Million cell updates/sec

Title: US-09-993-399-1

Perfect score: 79

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Searched: 225428 seqs, 4402918 residues

Total number of hits satisfying chosen parameters: 225428

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Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1000 summaries

Database : Published Applications AA New:

- 1: /SIDSS/ptodata/1/pubppa/US08_NEW_PUB pep.*
- 2: /SIDSS/ptodata/1/pubppa/US06_NEW_PUB pep.*
- 3: /SIDSS/ptodata/1/pubppa/US07_NEW_PUB pep.*
- 4: /SIDSS/ptodata/1/pubppa/US09_NEW_PUB pep.*
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- 7: /SIDSS/ptodata/1/pubppa/US12_NEW_PUB pep.*
- 8: /SIDSS/ptodata/1/pubppa/US13_NEW_PUB pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	79	100.0	2668	7	US-11-124-368A-215
3	51	64.6	726	7	US-11-096-568A-215
4	51	64.6	743	7	US-11-096-568A-216
5	51	64.6	829	7	US-11-096-568A-217
6	51	64.6	834	7	US-11-096-568A-218
7	51	64.6	851	7	US-11-096-568A-219
8	51	64.6	862	7	US-11-096-568A-220
9	46	58.2	811	7	US-11-096-568A-221
10	46	58.2	898	7	US-11-096-568A-222
11	46	58.2	932	7	US-11-096-568A-223
12	45	57.0	315	7	US-11-045-004-555
13	45	57.0	324	7	US-11-051-720-1349
14	45	57.0	385	7	US-11-051-720-1348
15	45	57.0	514	7	US-11-051-720-1346
16	45	57.0	737	7	US-11-051-720-1345
17	45	57.0	911	6	US-10-330-773-712
18	45	57.0	952	6	US-10-330-773-709
19	45	57.0	957	7	US-11-051-720-1338
20	44	55.7	292	7	US-11-096-568A-26779
21	44	55.7	331	7	US-11-096-568A-26778
22	44	55.7	338	7	US-11-096-568A-26777
23	44	55.7	799	7	US-11-096-568A-26771
24	44	55.7	808	7	US-11-096-568A-26949
25	44	55.7	842	7	US-11-096-568A-26770

26	44	55.7	849	7	US-11-096-568A-26769	Sequence 26769, A
27	44	55.7	897	7	US-11-096-568A-26948	Sequence 26948, A
28	43	54.4	975	7	US-11-096-568A-27943	Sequence 27943, A
29	43	54.4	983	7	US-11-096-568A-27942	Sequence 27942, A
30	43	54.4	1039	7	US-11-096-568A-30324	Sequence 30324, A
31	43	54.4	1055	7	US-11-096-568A-30323	Sequence 30323, A
32	43	54.4	1063	7	US-11-096-568A-30322	Sequence 30322, A
33	43	54.4	1087	7	US-11-096-568A-27941	Sequence 27941, A
34	41	51.9	970	7	US-11-096-568A-34153	Sequence 34153, A
35	41	51.9	1035	7	US-11-096-568A-34152	Sequence 34152, A
36	41	51.9	1042	7	US-11-096-568A-34151	Sequence 34151, A
37	40	50.6	302	7	US-11-082-389-84	Sequence 84, Appl
38	40	50.6	1142	7	US-11-079-463-10327	Sequence 3831, Ap
39	38	48.1	453	7	US-11-079-463-10327	Sequence 10327, A
40	38	48.1	506	7	US-11-188-298-19543	Sequence 19543, A
41	37	46.8	290	6	US-10-506-454-292	Sequence 292, App
42	37	46.8	334	7	US-11-098-686-11287	Sequence 11287, A
43	37	46.8	353	7	US-11-098-686-10227	Sequence 10227, A
44	37	46.8	575	7	US-11-087-099-422	Sequence 422, App
45	37	46.8	1145	7	US-11-096-568A-29274	Sequence 29274, A
46	37	46.8	1160	7	US-11-096-568A-29273	Sequence 29273, A
47	37	46.8	1195	7	US-11-096-568A-29272	Sequence 29272, A
48	36	45.6	204	7	US-11-045-004-1154	Sequence 1154, Ap
49	36	45.6	313	7	US-11-188-298-20356	Sequence 20356, A
50	36	45.6	317	7	US-11-153-569-12	Sequence 12, Appl
51	36	45.6	384	7	US-11-187-571-2	Sequence 2, Appl
52	36	45.6	411	7	US-11-188-298-10624	Sequence 10624, A
53	36	45.6	750	7	US-11-096-568A-18049	Sequence 18049, A
54	36	45.6	802	7	US-11-096-568A-18048	Sequence 18048, A
55	36	45.6	823	7	US-11-096-568A-18047	Sequence 18047, A
56	36	45.6	1493	6	US-10-330-773-502	Sequence 502, App
57	36	45.6	1826	6	US-10-330-773-499	Sequence 499, App
58	35	44.3	194	6	US-10-986-501-341	Sequence 341, App
59	35	44.3	340	7	US-11-145-532-5	Sequence 5, Appl
60	35	44.3	340	7	US-11-145-532-21	Sequence 21, Appl
61	35	44.3	389	7	US-11-188-298-16747	Sequence 16747, A
62	35	44.3	391	7	US-11-096-568A-22689	Sequence 22689, A
63	35	44.3	392	7	US-11-188-298-6028	Sequence 6028, Ap
64	35	44.3	411	7	US-11-188-298-18419	Sequence 18419, A
65	35	44.3	412	7	US-11-188-298-11847	Sequence 11847, A
66	35	44.3	440	7	US-11-096-568A-22688	Sequence 22688, A
67	35	44.3	444	7	US-11-096-568A-22687	Sequence 22687, A
68	35	44.3	632	6	US-10-063-703-40	Sequence 40, Appl
69	35	44.3	632	6	US-10-194-487-166	Sequence 166, App
70	35	44.3	632	6	US-10-195-883-166	Sequence 166, App
71	35	44.3	632	6	US-10-195-888-166	Sequence 166, App
72	35	44.3	632	6	US-10-195-889-166	Sequence 166, App
73	35	44.3	632	7	US-11-102-240-40	Sequence 40, Appl
74	35	44.3	632	7	US-11-103-195-40	Sequence 40, Appl
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76	35	44.3	660	6	US-10-973-115B-480	Sequence 480, App
77	35	44.3	660	6	US-11-290-153-480	Sequence 480, App
78	35	44.3	746	7	US-11-024-959-346	Sequence 346, App
79	35	44.3	746	7	US-11-079-463-8339	Sequence 8339, Ap
80	35	44.3	746	7	US-11-082-544-60	Sequence 60, Appl
81	34	43.0	140	7	US-11-082-544-60	Sequence 60, Appl
82	34	43.0	214	7	US-11-188-298-9521	Sequence 9521, Ap
83	34	43.0	214	7	US-11-188-298-9651	Sequence 9651, Ap
84	34	43.0	215	7	US-11-096-568A-20683	Sequence 20683, A
85	34	43.0	302	7	US-11-087-099-1820	Sequence 1820, Ap
86	34	43.0	302	7	US-11-188-298-2559	Sequence 2559, Ap
87	34	43.0	302	7	US-11-188-298-6674	Sequence 6674, Ap
88	34	43.0	401	7	US-11-188-298-10358	Sequence 10358, A
89	34	43.0	414	7	US-11-096-568A-32139	Sequence 32139, A
90	34	43.0	414	7	US-11-188-298-21422	Sequence 21422, A
91	34	43.0	472	7	US-11-096-568A-32138	Sequence 32138, A
92	34	43.0	472	7	US-11-188-298-6721	Sequence 6721, Ap
93	34	43.0	494	7	US-11-096-568A-32137	Sequence 32137, A
94	34	43.0	498	6	US-10-204-639-37	Sequence 37, Appl
95	34	43.0	542	6	US-10-858-730-106	Sequence 106, App
96	34	43.0	640	7	US-11-087-099-2757	Sequence 2757, Ap
97	34	43.0	798	7	US-11-072-512-3335	Sequence 3335, Ap
98	34	43.0	1267	7	US-11-109-156-35	Sequence 35, Appl

99	34	43.0	1653	6	US-10-453-372-866	Sequence 866, App	172	32	40.5	486	7	US-11-096-568A-28698	Sequence 28698, A
100	34	43.0	2340	7	US-11-052-554A-171	Sequence 171, App	173	32	40.5	494	7	US-11-096-568A-28697	Sequence 28697, A
101	33.5	42.4	131	7	US-11-045-004-2632	Sequence 2632, App	174	32	40.5	500	6	US-10-467-657-3344	Sequence 3344, App
102	33.5	42.4	320	6	US-10-995-561-947	Sequence 947, App	175	32	40.5	515	7	US-11-096-568A-28696	Sequence 28696, A
103	32.5	42.4	372	6	US-10-844-035-1	Sequence 1, Appl	176	32	40.5	534	7	US-11-096-568A-14686	Sequence 14686, A
104	33.5	42.4	373	6	US-10-995-561-948	Sequence 948, App	177	32	40.5	534	7	US-11-096-568A-32514	Sequence 32514, A
105	33.5	42.4	375	6	US-10-995-561-946	Sequence 946, App	178	32	40.5	534	7	US-11-096-568A-32513	Sequence 32513, A
106	33.5	42.4	385	6	US-10-995-561-945	Sequence 945, App	179	32	40.5	567	7	US-11-052-554A-129	Sequence 129, App
107	33.5	42.4	385	6	US-10-995-561-949	Sequence 949, App	180	32	40.5	572	7	US-11-113-837-4	Sequence 4, Appl
108	33.5	42.4	399	7	US-11-045-004-1683	Sequence 1683, App	181	32	40.5	637	7	US-11-096-568A-32512	Sequence 32512, A
109	33	41.8	117	6	US-10-507-662-46	Sequence 46, Appl	182	32	40.5	714	7	US-11-094-917-33	Sequence 33, Appl
110	33	41.8	110	6	US-11-077-619-76	Sequence 76, Appl	183	32	40.5	752	7	US-11-055-822-912	Sequence 912, App
111	33	41.8	126	6	US-10-507-662-19	Sequence 19, Appl	184	32	40.5	762	7	US-11-109-157A-6	Sequence 6, Appl
112	33	41.8	222	7	US-11-096-568A-11051	Sequence 12051, A	185	32	40.5	785	7	US-11-079-463-7729	Sequence 7729, App
113	33	41.8	224	7	US-11-096-568A-19010	Sequence 19010, A	186	32	40.5	811	7	US-11-045-004-126	Sequence 126, App
114	33	41.8	247	7	US-11-087-099-6223	Sequence 6223, App	187	32	40.5	875	7	US-11-096-568A-29796	Sequence 29796, A
115	33	41.8	247	7	US-11-188-298-16722	Sequence 16722, A	188	32	40.5	887	7	US-11-188-298-4356	Sequence 4356, App
116	33	41.8	249	6	US-10-527-500-25	Sequence 25, Appl	189	32	40.5	896	7	US-11-096-568A-29795	Sequence 29795, A
117	33	41.8	252	7	US-11-098-686-11048	Sequence 11048, A	190	32	40.5	917	7	US-11-108-864-19	Sequence 19, Appl
118	33	41.8	271	7	US-11-096-568A-19009	Sequence 19009, A	191	32	40.5	934	7	US-11-096-568A-29794	Sequence 29794, A
119	33	41.8	330	7	US-11-074-176-174	Sequence 174, App	192	32	40.5	961	7	US-11-062	Sequence 5, Appl
120	33	41.8	330	7	US-11-087-099-2823	Sequence 2823, App	193	32	40.5	1059	7	US-11-062	Sequence 6, Appl
121	33	41.8	330	7	US-11-087-099-7121	Sequence 7121, App	194	32	40.5	1067	7	US-11-062	Sequence 7, Appl
122	33	41.8	338	7	US-11-045-004-862	Sequence 862, App	195	32	40.5	1070	7	US-11-109-157A-5	Sequence 5, Appl
123	33	41.8	362	7	US-11-096-568A-13008	Sequence 13008, A	196	32	40.5	1076	7	US-11-062	Sequence 4, Appl
124	33	41.8	362	7	US-11-186-284-123	Sequence 123, App	197	32	40.5	1084	7	US-11-062	Sequence 8, Appl
125	33	41.8	490	7	US-11-188-298-9166	Sequence 9166, App	198	32	40.5	1092	7	US-11-062	Sequence 6, Appl
126	33	41.8	502	7	US-11-188-298-19312	Sequence 19312, A	199	32	40.5	1095	7	US-11-062	Sequence 7, Appl
127	33	41.8	511	7	US-11-045-004-42	Sequence 42, Appl	200	32	40.5	1122	6	US-10-330-773-260	Sequence 260, App
128	33	41.8	535	6	US-10-131-826A-124	Sequence 124, App	201	32	40.5	1152	7	US-11-080-026-4	Sequence 4, Appl
129	33	41.8	535	6	US-10-973-115B-124	Sequence 124, App	202	32	40.5	1786	7	US-11-188-298-4785	Sequence 4785, App
130	33	41.8	535	6	US-11-290-153-124	Sequence 124, App	203	32	40.5	1907	7	US-11-039-398-25	Sequence 25, Appl
131	33	41.8	684	7	US-11-079-463-10136	Sequence 10136, A	204	32	40.5	2556	7	US-11-050-346-67	Sequence 67, Appl
132	33	41.8	896	7	US-11-188-298-8754	Sequence 8754, App	205	31.5	39.9	320	6	US-10-453-372-854	Sequence 854, App
133	33	41.8	906	7	US-11-087-099-11997	Sequence 11997, A	206	31.5	39.9	844	6	US-10-453-372-852	Sequence 852, App
134	33	41.8	922	7	US-11-072-512-2694	Sequence 2694, App	207	31.5	39.9	844	6	US-10-453-372-856	Sequence 856, App
135	33	41.8	934	7	US-11-052-554A-10	Sequence 10, Appl	208	31.5	39.9	905	6	US-10-330-773-873	Sequence 873, App
136	32	40.5	17	6	US-10-507-662-4	Sequence 4, Appl	209	31.5	39.9	938	7	US-11-072-512-3855	Sequence 3855, App
137	32	40.5	20	7	US-11-188-187A-32	Sequence 32, Appl	210	31	39.2	14	7	US-11-116-144-184	Sequence 184, App
138	32	40.5	49	6	US-10-467-657-4194	Sequence 4194, App	211	31	39.2	14	7	US-11-220-372-184	Sequence 184, App
139	32	40.5	126	6	US-10-507-662-20	Sequence 20, Appl	212	31	39.2	59	7	US-11-096-568A-561	Sequence 561, App
140	32	40.5	126	6	US-10-507-662-21	Sequence 21, Appl	213	31	39.2	91	6	US-10-485-788A-652	Sequence 652, App
141	32	40.5	130	7	US-11-188-187A-3	Sequence 3, Appl	214	31	39.2	91	7	US-11-053-076-124	Sequence 124, App
142	32	40.5	222	6	US-10-793-626-376	Sequence 376, App	215	31	39.2	122	6	US-10-506-454-1174	Sequence 1174, App
143	32	40.5	250	6	US-10-467-657-3132	Sequence 3132, App	216	31	39.2	148	7	US-11-098-686-101	Sequence 101, App
144	32	40.5	252	7	US-11-096-568A-1494	Sequence 1494, App	217	31	39.2	172	7	US-11-096-568A-4476	Sequence 4476, App
145	32	40.5	257	7	US-11-096-568A-1493	Sequence 1493, App	218	31	39.2	173	7	US-11-096-568A-4475	Sequence 4475, App
146	32	40.5	264	7	US-11-096-568A-1492	Sequence 1492, App	219	31	39.2	189	7	US-11-096-568A-34078	Sequence 34078, A
147	32	40.5	287	6	US-10-976-016-1	Sequence 1, Appl	220	31	39.2	202	7	US-11-123-241-50	Sequence 50, Appl
148	32	40.5	308	7	US-11-188-298-3745	Sequence 3745, App	221	31	39.2	208	7	US-11-079-463-7850	Sequence 7850, App
149	32	40.5	308	7	US-11-188-298-10390	Sequence 10390, A	222	31	39.2	215	7	US-11-079-463-5285	Sequence 5285, App
150	32	40.5	315	7	US-11-096-568A-20497	Sequence 20497, A	223	31	39.2	226	7	US-11-096-568A-29157	Sequence 29157, A
151	32	40.5	348	7	US-11-045-004-2586	Sequence 2586, App	224	31	39.2	229	7	US-11-079-463-7985	Sequence 7985, App
152	32	40.5	362	7	US-11-109-157A-8	Sequence 8, Appl	225	31	39.2	236	7	US-11-054-281-118	Sequence 118, App
153	32	40.5	362	7	US-11-072-512-2732	Sequence 2732, App	226	31	39.2	237	6	US-10-510-386-34	Sequence 34, Appl
154	32	40.5	370	7	US-11-109-157A-41	Sequence 41, Appl	227	31	39.2	248	7	US-11-096-568A-29278	Sequence 29278, A
155	32	40.5	376	6	US-11-072-512-2623	Sequence 2623, App	228	31	39.2	255	7	US-11-096-568A-29125	Sequence 29125, A
156	32	40.5	387	6	US-10-501-035-213	Sequence 213, App	229	31	39.2	269	7	US-11-055-822-282	Sequence 282, App
157	32	40.5	394	6	US-10-821-234-1194	Sequence 1194, App	230	31	39.2	269	7	US-11-055-822-618	Sequence 618, App
158	32	40.5	414	7	US-11-096-568A-14688	Sequence 14688, A	231	31	39.2	271	7	US-11-055-822-280	Sequence 280, App
159	32	40.5	427	7	US-11-096-568A-14687	Sequence 14687, A	232	31	39.2	271	7	US-11-055-822-616	Sequence 616, App
160	32	40.5	434	6	US-10-915-002-216	Sequence 216, Appl	233	31	39.2	275	7	US-11-087-099-6624	Sequence 6624, App
161	32	40.5	437	6	US-10-850-465-2	Sequence 2, Appl	234	31	39.2	282	7	US-11-096-568A-29156	Sequence 29156, A
162	32	40.5	441	7	US-11-087-099-10304	Sequence 10304, A	235	31	39.2	289	7	US-11-087-099-8567	Sequence 8567, App
163	32	40.5	441	7	US-11-087-099-11270	Sequence 11270, A	236	31	39.2	293	7	US-11-116-939-10	Sequence 10, Appl
164	32	40.5	446	7	US-11-096-568A-27457	Sequence 27457, A	237	31	39.2	293	7	US-11-098-686-10616	Sequence 10616, A
165	32	40.5	451	7	US-11-096-568A-1960	Sequence 1960, App	238	31	39.2	304	7	US-11-096-568A-29277	Sequence 29277, A
166	32	40.5	451	7	US-11-096-568A-27456	Sequence 27456, A	239	31	39.2	311	7	US-11-096-568A-29124	Sequence 29124, A
167	32	40.5	459	7	US-11-087-099-1361	Sequence 1361, App	240	31	39.2	312	7	US-11-054-281-32	Sequence 32, Appl
168	32	40.5	464	7	US-11-172-740-2137	Sequence 2137, App	241	31	39.2	312	7	US-11-054-281-320	Sequence 320, App
169	32	40.5	475	7	US-11-188-298-14237	Sequence 14237, App	242	31	39.2	312	7	US-11-054-281-324	Sequence 324, App
170	32	40.5	475	7	US-11-096-568A-27455	Sequence 27455, A	243	31	39.2	312	7	US-11-072-512-2822	Sequence 2822, App
171	32	40.5	485	7	US-11-188-298-10345	Sequence 10345, A	244	31	39.2	320	7	US-11-096-568A-29155	Sequence 29155, A

245	31	39.2	330	7	US-11-087-099-10594	Sequence 10594, A	318	30	38.0	17	7	US-11-097-812-91	Sequence 91, Appl
246	31	39.2	336	5	US-09-995-493-230	Sequence 230, Appl	319	30	38.0	18	7	US-11-145-861-173	Sequence 173, Appl
247	31	39.2	336	7	US-11-096-568A-33747	Sequence 33747, A	320	30	38.0	33	6	US-10-895-064-1334	Sequence 1334, Ap
248	31	39.2	342	7	US-11-096-568A-29276	Sequence 29276, A	321	30	38.0	33	7	US-11-129-741-1334	Sequence 1334, Ap
249	31	39.2	342	7	US-11-096-568A-33746	Sequence 33746, A	322	30	38.0	33	6	US-10-467-657-1510	Sequence 1510, Ap
250	31	39.2	343	7	US-11-096-568A-33745	Sequence 33745, A	323	30	38.0	64	6	US-10-467-657-632	Sequence 632, Appl
251	31	39.2	346	7	US-11-079-463-9218	Sequence 9218, A	324	30	38.0	64	6	US-10-475-075-790	Sequence 790, Appl
252	31	39.2	349	7	US-11-096-568A-29123	Sequence 29123, A	325	30	38.0	76	7	US-11-172-571-28	Sequence 28, Appl
253	31	39.2	357	7	US-11-188-298-486	Sequence 486, Appl	326	30	38.0	100	7	US-11-045-004-2684	Sequence 2684, Ap
254	31	39.2	386	7	US-11-096-568A-26027	Sequence 26027, A	327	30	38.0	119	7	US-11-097-812-72	Sequence 72, Appl
255	31	39.2	388	7	US-11-096-568A-26026	Sequence 26026, A	328	30	38.0	119	7	US-11-097-812-81	Sequence 81, Appl
256	31	39.2	389	6	US-10-513-118-2	Sequence 2, Appli	329	30	38.0	135	6	US-10-330-773-528	Sequence 528, Appl
257	31	39.2	391	7	US-11-087-099-4808	Sequence 4808, Ap	330	30	38.0	145	6	US-10-330-773-530	Sequence 530, Appl
258	31	39.2	392	7	US-11-087-099-8324	Sequence 8324, Ap	331	30	38.0	163	7	US-11-188-298-11871	Sequence 11871, A
259	31	39.2	399	6	US-10-853-533-3	Sequence 3, Appli	332	30	38.0	167	7	US-11-234-786-481	Sequence 481, Appl
260	31	39.2	403	6	US-10-983-011-2	Sequence 2, Appli	333	30	38.0	168	6	US-10-821-234-1426	Sequence 1426, Ap
261	31	39.2	403	7	US-11-109-156-29	Sequence 29, Appl	334	30	38.0	174	6	US-10-991-285-874	Sequence 874, Appl
262	31	39.2	409	6	US-10-467-657-4320	Sequence 4208, Ap	335	30	38.0	176	6	US-10-330-773-525	Sequence 525, Appl
263	31	39.2	409	6	US-10-467-657-7088	Sequence 7088, Ap	336	30	38.0	179	7	US-11-079-463-6974	Sequence 6974, Ap
264	31	39.2	409	7	US-11-188-298-3056	Sequence 3056, Ap	337	30	38.0	186	7	US-11-087-099-3432	Sequence 3432, Ap
265	31	39.2	409	7	US-11-188-298-18383	Sequence 18383, A	338	30	38.0	192	7	US-11-087-099-9855	Sequence 9855, Ap
266	31	39.2	412	7	US-11-116-939-12	Sequence 12, Appl	339	30	38.0	192	7	US-11-087-099-11223	Sequence 11223, A
267	31	39.2	412	7	US-11-188-298-574	Sequence 574, Appl	340	30	38.0	196	7	US-11-172-740-2035	Sequence 2035, Ap
268	31	39.2	420	7	US-11-188-298-10248	Sequence 10248, A	341	30	38.0	205	7	US-11-087-099-2318	Sequence 2318, Ap
269	31	39.2	421	7	US-11-188-298-7320	Sequence 7320, Ap	342	30	38.0	221	7	US-11-170-653-20	Sequence 20, Appl
270	31	39.2	423	6	US-10-853-533-2	Sequence 2, Appli	343	30	38.0	221	7	US-11-087-099-2693	Sequence 2693, Ap
271	31	39.2	423	7	US-11-008-570-30	Sequence 30, Appl	344	30	38.0	222	7	US-11-045-004-2607	Sequence 2607, Ap
272	31	39.2	437	7	US-11-096-568A-26025	Sequence 26025, A	345	30	38.0	227	7	US-11-170-653-21	Sequence 21, Appl
273	31	39.2	445	7	US-11-072-512-2209	Sequence 2209, Ap	346	30	38.0	227	7	US-11-170-653-22	Sequence 22, Appl
274	31	39.2	449	7	US-11-188-298-14638	Sequence 14638, A	347	30	38.0	243	7	US-11-188-298-8625	Sequence 8625, Ap
275	31	39.2	459	7	US-11-188-298-18157	Sequence 18157, A	348	30	38.0	244	7	US-11-188-298-6364	Sequence 6364, Ap
276	31	39.2	469	7	US-11-188-298-15973	Sequence 15973, A	349	30	38.0	245	7	US-11-087-099-8114	Sequence 8114, Ap
277	31	39.2	472	7	US-11-188-298-8005	Sequence 8005, Ap	350	30	38.0	247	6	US-10-467-657-7320	Sequence 7320, Ap
278	31	39.2	472	7	US-11-188-298-20912	Sequence 20912, A	351	30	38.0	249	7	US-11-172-740-2235	Sequence 2235, Ap
279	31	39.2	478	7	US-11-188-298-17361	Sequence 17361, A	352	30	38.0	250	6	US-10-793-626-2310	Sequence 2310, Ap
280	31	39.2	487	7	US-11-188-298-3772	Sequence 3772, Ap	353	30	38.0	266	7	US-11-234-786-534	Sequence 534, Appl
281	31	39.2	488	7	US-11-188-298-6013	Sequence 6013, Ap	354	30	38.0	273	6	US-10-793-626-608	Sequence 608, Appl
282	31	39.2	504	7	US-11-188-298-14675	Sequence 14675, A	355	30	38.0	274	7	US-11-188-298-17507	Sequence 17507, A
283	31	39.2	507	7	US-11-033-039-96	Sequence 96, Appl	356	30	38.0	274	7	US-11-188-298-19272	Sequence 19272, A
284	31	39.2	510	7	US-11-188-298-5258	Sequence 5258, Ap	357	30	38.0	282	7	US-11-183-205-40	Sequence 40, Appl
285	31	39.2	516	7	US-11-188-298-17942	Sequence 17942, A	358	30	38.0	288	7	US-11-087-099-11574	Sequence 11574, A
286	31	39.2	517	7	US-11-188-298-2805	Sequence 2805, Ap	359	30	38.0	293	7	US-11-096-568A-10770	Sequence 10770, A
287	31	39.2	518	7	US-11-188-298-20809	Sequence 20809, A	360	30	38.0	296	7	US-11-087-099-1580	Sequence 1580, Ap
288	31	39.2	525	7	US-11-188-298-3625	Sequence 3625, Ap	361	30	38.0	299	7	US-11-087-099-1439	Sequence 1439, Ap
289	31	39.2	546	7	US-11-188-298-16801	Sequence 16801, A	362	30	38.0	299	7	US-11-087-099-9542	Sequence 9542, Ap
290	31	39.2	552	6	US-10-467-657-4142	Sequence 4142, Ap	363	30	38.0	300	7	US-11-087-099-1528	Sequence 1528, Ap
291	31	39.2	558	6	US-10-506-454-972	Sequence 972, Appl	364	30	38.0	308	7	US-11-188-298-15926	Sequence 15926, A
292	31	39.2	580	7	US-11-045-004-2746	Sequence 2746, Ap	365	30	38.0	308	7	US-11-188-298-20337	Sequence 20337, A
293	31	39.2	659	6	US-10-793-626-1596	Sequence 1596, Ap	366	30	38.0	314	7	US-11-096-568A-2465	Sequence 2465, Ap
294	31	39.2	671	7	US-11-096-568A-28178	Sequence 28178, A	367	30	38.0	317	6	US-10-873-528-85	Sequence 65, Appl
295	31	39.2	672	7	US-11-096-568A-28177	Sequence 28177, A	368	30	38.0	326	7	US-11-087-099-731	Sequence 731, Appl
296	31	39.2	704	7	US-11-232-440-49	Sequence 49, Appl	369	30	38.0	326	7	US-11-087-099-2404	Sequence 2404, Ap
297	31	39.2	715	7	US-11-096-568A-28176	Sequence 28176, A	370	30	38.0	326	7	US-11-087-099-9532	Sequence 9532, Ap
298	31	39.2	746	7	US-11-072-175-169	Sequence 169, Appl	371	30	38.0	327	7	US-11-087-099-10124	Sequence 10124, A
299	31	39.2	824	7	US-11-116-933-11	Sequence 11, Appl	372	30	38.0	327	7	US-11-045-004-2672	Sequence 2672, Ap
300	31	39.2	1144	6	US-10-467-657-1820	Sequence 1820, Ap	373	30	38.0	328	7	US-11-087-099-4727	Sequence 4727, Ap
301	31	39.2	1190	7	US-11-043-889-20	Sequence 20, Appl	374	30	38.0	328	7	US-11-087-099-7553	Sequence 7553, Ap
302	31	39.2	1212	6	US-10-501-035-374	Sequence 374, Appl	375	30	38.0	329	7	US-11-087-099-1058	Sequence 1058, Ap
303	31	39.2	3748	7	US-11-132-686-8	Sequence 8, Appli	376	30	38.0	329	7	US-11-087-099-6155	Sequence 6155, Ap
304	31	39.2	3749	7	US-11-132-686-6	Sequence 6, Appli	377	30	38.0	329	7	US-11-087-099-9296	Sequence 9296, Ap
305	31	39.2	3749	7	US-11-132-686-12	Sequence 12, Appl	378	30	38.0	329	7	US-11-087-099-11934	Sequence 11934, A
306	31	39.2	3912	7	US-11-132-686-7	Sequence 7, Appli	379	30	38.0	330	7	US-11-087-099-6398	Sequence 6398, Ap
307	31	39.2	3913	7	US-11-132-686-5	Sequence 5, Appli	380	30	38.0	330	7	US-11-087-099-9899	Sequence 9899, Ap
308	31	39.2	3913	7	US-11-132-686-9	Sequence 9, Appli	381	30	38.0	334	7	US-11-087-099-7131	Sequence 7131, Ap
309	30.5	38.6	89	7	US-11-079-463-6577	Sequence 6577, Ap	382	30	38.0	345	7	US-11-188-298-13763	Sequence 13763, A
310	30.5	38.6	191	7	US-11-096-568A-33331	Sequence 33331, A	383	30	38.0	349	7	US-11-096-568A-2464	Sequence 2464, Ap
311	30.5	38.6	210	7	US-11-096-568A-33330	Sequence 33330, A	384	30	38.0	365	7	US-11-087-099-3375	Sequence 3375, Ap
312	30.5	38.6	233	7	US-11-096-568A-33329	Sequence 33329, A	385	30	38.0	375	6	US-10-469-469-115	Sequence 115, Appl
313	30.5	38.6	296	7	US-11-078-280-2	Sequence 2, Appli	386	30	38.0	378	7	US-11-087-099-12205	Sequence 12205, A
314	30.5	38.6	299	6	US-10-194-487-164	Sequence 164, Appl	387	30	38.0	380	7	US-11-150-845-44	Sequence 44, Appl
315	30.5	38.6	299	6	US-10-195-883-164	Sequence 164, Appl	388	30	38.0	380	7	US-11-150-487-38	Sequence 38, Appl
316	30.5	38.6	299	6	US-10-195-888-164	Sequence 164, Appl	389	30	38.0	387	7	US-11-010-795-5	Sequence 5, Appl
317	30.5	38.6	299	6	US-10-195-889-164	Sequence 164, Appl	390	30	38.0	387	7	US-11-010-795-14	Sequence 14, Appl

391	30	38.0	387	7	US-11-010-795-18	Sequence 18, Appl	464	29.5	37.3	186	6	US-10-667-295-166	Sequence 166, App
392	30	38.0	390	7	US-11-188-298-7867	Sequence 7867, Ap	465	29.5	37.3	186	6	US-10-667-295-199	Sequence 199, App
393	30	38.0	411	7	US-11-188-298-1737	Sequence 1737, Ap	466	29.5	37.3	186	7	US-11-172-740-2097	Sequence 2097, Ap
394	30	38.0	414	7	US-11-087-099-2837	Sequence 2837, Ap	467	29.5	37.3	199	7	US-11-045-004-1026	Sequence 1026, Ap
395	30	38.0	429	7	US-11-188-298-12329	Sequence 12329, A	468	29.5	37.3	204	6	US-10-667-295-165	Sequence 165, App
396	30	38.0	432	7	US-11-188-298-5835	Sequence 5835, Ap	469	29.5	37.3	204	6	US-10-667-295-198	Sequence 198, App
397	30	38.0	454	7	US-11-089-551A-35	Sequence 35, Appl	470	29.5	37.3	204	6	US-11-172-740-2092	Sequence 2092, Ap
398	30	38.0	456	7	US-11-188-298-2769	Sequence 2769, Ap	471	29.5	37.3	204	7	US-11-172-740-2093	Sequence 2093, Ap
399	30	38.0	490	7	US-11-096-568A-31601	Sequence 31601, A	472	29.5	37.3	204	7	US-11-172-740-2094	Sequence 2094, Ap
400	30	38.0	492	7	US-11-188-298-14410	Sequence 14410, A	473	29.5	37.3	204	7	US-11-172-740-2095	Sequence 2095, Ap
401	30	38.0	492	7	US-11-188-298-18524	Sequence 18524, A	474	29.5	37.3	204	7	US-11-172-740-2096	Sequence 2096, Ap
402	30	38.0	496	7	US-11-096-568A-31600	Sequence 31600, A	475	29.5	37.3	204	7	US-11-172-740-2098	Sequence 2098, Ap
403	30	38.0	497	7	US-11-188-298-9664	Sequence 9664, Ap	476	29.5	37.3	227	6	US-10-667-295-197	Sequence 197, App
404	30	38.0	499	7	US-11-096-568A-15796	Sequence 15796, A	477	29.5	37.3	298	7	US-11-096-568A-3265	Sequence 3265, Ap
405	30	38.0	510	7	US-11-031-206-80	Sequence 80, Appl	478	29.5	37.3	298	7	US-11-096-568A-3266	Sequence 3266, Ap
406	30	38.0	517	7	US-11-098-686-11247	Sequence 11247, A	479	29.5	37.3	303	7	US-11-096-568A-3264	Sequence 3264, Ap
407	30	38.0	517	7	US-11-096-568A-15795	Sequence 15795, A	480	29.5	37.3	307	7	US-11-096-568A-3263	Sequence 3263, Ap
408	30	38.0	534	7	US-11-096-568A-31599	Sequence 31599, A	481	29.5	37.3	307	7	US-11-045-004-2693	Sequence 2693, Ap
409	30	38.0	559	6	US-10-521-162-4	Sequence 4, Appl	482	29.5	37.3	396	7	US-11-087-099-544	Sequence 544, App
410	30	38.0	560	6	US-10-995-561-1026	Sequence 1026, Ap	483	29.5	37.3	482	7	US-11-232-440-33	Sequence 33, Appl
411	30	38.0	566	7	US-11-188-298-6791	Sequence 6791, Ap	484	29.5	37.3	974	6	US-10-330-773-944	Sequence 944, App
412	30	38.0	566	7	US-11-188-298-22197	Sequence 22197, A	485	29.5	37.3	1164	7	US-11-087-099-2278	Sequence 2278, Ap
413	30	38.0	580	7	US-11-143-984A-30	Sequence 30, Appl	486	29.5	37.3	1164	7	US-11-087-099-9070	Sequence 9070, Ap
414	30	38.0	584	7	US-11-072-175-157	Sequence 157, App	487	29	36.7	25	7	US-11-083-624-44	Sequence 44, Appl
415	30	38.0	614	7	US-11-150-845-34	Sequence 34, Appl	488	29	36.7	25	7	US-11-223-699A-42	Sequence 42, Appl
416	30	38.0	614	7	US-11-150-487-34	Sequence 34, Appl	489	29	36.7	25	7	US-11-121-566A-42	Sequence 42, Appl
417	30	38.0	616	6	US-10-995-561-1018	Sequence 1018, Ap	490	29	36.7	35	7	US-11-083-624-55	Sequence 55, Appl
418	30	38.0	616	6	US-10-995-561-1022	Sequence 1022, Ap	491	29	36.7	35	7	US-11-037-199-46	Sequence 46, Appl
419	30	38.0	617	7	US-11-150-845-46	Sequence 46, Appl	492	29	36.7	139	7	US-11-004-399-3152	Sequence 3152, Ap
420	30	38.0	617	7	US-11-150-487-40	Sequence 40, Appl	493	29	36.7	53	6	US-10-914-391A-7	Sequence 7, Appl
421	30	38.0	638	7	US-11-087-099-1176	Sequence 1176, Ap	494	29	36.7	79	7	US-11-086-568A-3415	Sequence 3415, Ap
422	30	38.0	688	7	US-11-098-686-10191	Sequence 10191, A	495	29	36.7	82	6	US-10-467-657-564	Sequence 564, App
423	30	38.0	690	6	US-10-131-826A-306	Sequence 306, App	496	29	36.7	92	6	US-10-821-234-1505	Sequence 1505, Ap
424	30	38.0	690	6	US-10-973-115B-306	Sequence 306, App	497	29	36.7	114	6	US-10-763-712A-51	Sequence 51, Appl
425	30	38.0	690	7	US-11-290-153-306	Sequence 306, App	498	29	36.7	121	7	US-11-188-298-22057	Sequence 22057, A
426	30	38.0	702	6	US-10-467-657-7230	Sequence 7230, Ap	499	29	36.7	137	6	US-10-527-500-47	Sequence 47, Appl
427	30	38.0	706	7	US-11-188-298-11914	Sequence 11914, A	500	29	36.7	145	7	US-11-088-570-62	Sequence 62, Appl
428	30	38.0	707	6	US-11-045-004-1281	Sequence 1281, Ap	501	29	36.7	157	6	US-10-467-657-5496	Sequence 5496, Ap
429	30	38.0	712	6	US-10-521-162-12	Sequence 12, Appl	502	29	36.7	161	7	US-11-087-099-10533	Sequence 10533, A
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431	30	38.0	732	6	US-10-518-599-23	Sequence 23, Appl	504	29	36.7	196	6	US-10-467-657-7254	Sequence 7254, Ap
432	30	38.0	732	6	US-10-995-561-1020	Sequence 1020, Ap	505	29	36.7	196	6	US-10-467-657-8130	Sequence 8130, Ap
433	30	38.0	738	7	US-11-188-298-2319	Sequence 2319, Ap	506	29	36.7	197	7	US-10-467-657-8130	Sequence 8130, Ap
434	30	38.0	757	6	US-10-491-468-6	Sequence 6, Appl	507	29	36.7	201	7	US-11-156-516-27	Sequence 27, Appl
435	30	38.0	777	7	US-11-087-099-5978	Sequence 5978, Ap	508	29	36.7	204	7	US-11-169-041-161	Sequence 161, App
436	30	38.0	798	7	US-11-188-298-9773	Sequence 9773, Ap	509	29	36.7	204	7	US-11-072-175-150	Sequence 150, App
437	30	38.0	804	7	US-11-070-080-18	Sequence 18, Appl	510	29	36.7	211	7	US-11-116-943-2	Sequence 2, Appl
438	30	38.0	817	7	US-11-098-686-11041	Sequence 11041, A	511	29	36.7	218	7	US-11-045-004-497	Sequence 497, App
439	30	38.0	820	6	US-10-467-657-4910	Sequence 4910, Ap	512	29	36.7	226	7	US-11-024-359-501	Sequence 501, App
440	30	38.0	827	7	US-10-463-5603	Sequence 5603, Ap	513	29	36.7	226	7	US-11-072-512-2138	Sequence 2138, Ap
441	30	38.0	883	7	US-11-079-463-5603	Sequence 1556, Ap	514	29	36.7	229	7	US-11-045-004-1183	Sequence 1183, Ap
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443	30	38.0	900	7	US-11-087-099-3766	Sequence 3766, Ap	516	29	36.7	253	7	US-11-054-515-860	Sequence 860, App
444	30	38.0	907	7	US-11-103-957-82	Sequence 82, Appl	517	29	36.7	253	7	US-11-096-568A-7429	Sequence 7429, Ap
445	30	38.0	912	6	US-10-467-657-7142	Sequence 7142, Ap	518	29	36.7	253	7	US-11-266-444-860	Sequence 860, App
446	30	38.0	915	7	US-11-087-099-6117	Sequence 6117, Ap	519	29	36.7	256	7	US-11-079-463-8557	Sequence 8557, App
447	30	38.0	920	7	US-11-087-099-11404	Sequence 11404, A	520	29	36.7	256	7	US-11-045-004-858	Sequence 858, App
448	30	38.0	920	7	US-11-188-298-21540	Sequence 21540, A	521	29	36.7	257	6	US-10-667-295-61	Sequence 61, Appl
449	30	38.0	932	7	US-11-079-463-6029	Sequence 6029, Ap	522	29	36.7	261	7	US-11-083-624-2	Sequence 2, Appl
450	30	38.0	937	7	US-11-079-463-7544	Sequence 7544, Ap	523	29	36.7	262	7	US-11-087-099-7815	Sequence 7815, Ap
451	30	38.0	965	7	US-11-079-463-5326	Sequence 5326, Ap	524	29	36.7	262	7	US-11-087-099-10891	Sequence 10891, A
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453	30	38.0	1100	7	US-11-045-004-2825	Sequence 2825, Ap	526	29	36.7	262	7	US-11-188-298-14411	Sequence 14411, A
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455	30	38.0	1302	6	US-10-995-561-1024	Sequence 1024, Ap	528	29	36.7	271	7	US-11-195-739-4	Sequence 4, Appl
456	30	38.0	1306	6	US-10-995-561-1027	Sequence 1027, Ap	529	29	36.7	276	7	US-11-087-099-5099	Sequence 5099, Ap
457	30	38.0	1375	6	US-10-995-561-809	Sequence 809, App	530	29	36.7	277	7	US-11-172-740-2183	Sequence 2183, Ap
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460	30	38.0	1730	7	US-11-096-568A-32050	Sequence 32050, A	533	29	36.7	286	7	US-11-172-740-115	Sequence 115, App
461	30	38.0	1757	7	US-11-096-568A-32049	Sequence 32049, A	534	29	36.7	286	7	US-11-172-740-2262	Sequence 2262, Ap
462	29.5	37.3	150	6	US-10-667-295-162	Sequence 162, App	535	29	36.7	288	7	US-11-045-004-1259	Sequence 1259, Ap
463	29.5	37.3	168	6	US-10-667-295-161	Sequence 161, App	536	29	36.7	289	7	US-11-096-568A-32768	Sequence 32768, A

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539	29	36.7	296	7	US-11-045-004-629	Sequence 629, App	612	29	36.7	422	7	US-11-188-298-19174	Sequence 19174, A
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542	29	36.7	301	7	US-11-172-740-1326	Sequence 1326, App	615	29	36.7	430	6	US-10-467-657-7448	Sequence 7448, App
543	29	36.7	304	6	US-10-793-626-1326	Sequence 650, App	616	29	36.7	431	7	US-11-096-568A-23163	Sequence 23163, A
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546	29	36.7	306	7	US-11-188-298-12363	Sequence 12363, A	619	29	36.7	450	7	US-11-188-298-9452	Sequence 9452, App
547	29	36.7	312	7	US-11-096-568A-32766	Sequence 32766, A	620	29	36.7	451	6	US-10-506-454-691	Sequence 691, App
548	29	36.7	312	7	US-11-045-004-1285	Sequence 1285, App	621	29	36.7	452	7	US-11-188-298-8497	Sequence 8497, App
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562	29	36.7	360	7	US-11-188-298-13249	Sequence 13249, A	635	29	36.7	485	7	US-11-172-740-2136	Sequence 2136, App
563	29	36.7	363	7	US-11-087-099-5458	Sequence 5458, App	636	29	36.7	485	7	US-11-188-298-313	Sequence 313, App
564	29	36.7	363	7	US-11-188-298-22281	Sequence 22281, A	637	29	36.7	487	7	US-11-188-298-6934	Sequence 6934, App
565	29	36.7	365	6	US-10-453-372-560	Sequence 560, App	638	29	36.7	490	7	US-11-096-568A-12370	Sequence 12370, A
566	29	36.7	368	7	US-11-096-568A-33732	Sequence 33732, A	639	29	36.7	492	6	US-10-467-9628-51	Sequence 51, Appl
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571	29	36.7	372	7	US-11-188-298-19827	Sequence 19827, A	644	29	36.7	522	6	US-10-467-657-7238	Sequence 7238, App
572	29	36.7	373	7	US-11-096-568A-23079	Sequence 23079, A	645	29	36.7	523	7	US-11-055-822-954	Sequence 954, App
573	29	36.7	373	7	US-11-096-568A-23165	Sequence 23165, A	646	29	36.7	535	7	US-11-188-298-13691	Sequence 13691, A
574	29	36.7	375	7	US-11-188-298-4639	Sequence 4639, App	647	29	36.7	537	7	US-11-098-686-11361	Sequence 11361, A
575	29	36.7	375	7	US-11-188-298-20720	Sequence 20720, A	648	29	36.7	549	7	US-11-194-246-431	Sequence 431, App
576	29	36.7	378	7	US-11-172-740-1329	Sequence 1329, App	649	29	36.7	550	7	US-11-113-837-17	Sequence 17, Appl
577	29	36.7	378	7	US-11-172-740-1335	Sequence 1335, App	650	29	36.7	554	7	US-11-000-463-240	Sequence 240, App
578	29	36.7	378	7	US-11-188-298-6856	Sequence 6856, App	651	29	36.7	563	6	US-10-878-556A-135	Sequence 135, App
579	29	36.7	378	7	US-11-188-298-15885	Sequence 15885, App	652	29	36.7	563	7	US-11-072-175-241	Sequence 241, App
580	29	36.7	379	7	US-11-096-568A-2989	Sequence 2989, App	653	29	36.7	585	7	US-11-188-298-6291	Sequence 6291, App
581	29	36.7	379	7	US-11-096-568A-2991	Sequence 2991, App	654	29	36.7	588	7	US-11-072-512-3053	Sequence 3053, App
582	29	36.7	380	6	US-10-204-639-39	Sequence 39, Appl	655	29	36.7	598	7	US-11-074-176-258	Sequence 258, App
583	29	36.7	382	7	US-11-096-568A-16256	Sequence 16256, A	656	29	36.7	607	7	US-11-096-568A-13814	Sequence 13814, A
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586	29	36.7	384	7	US-11-096-568A-33730	Sequence 33730, A	659	29	36.7	624	7	US-11-079-463-10187	Sequence 10187, A
587	29	36.7	389	7	US-11-096-568A-19737	Sequence 19737, A	660	29	36.7	633	7	US-11-119-683-3	Sequence 3, Appl
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591	29	36.7	392	7	US-11-188-298-19545	Sequence 19545, A	664	29	36.7	685	7	US-11-096-568A-33956	Sequence 33956, A
592	29	36.7	393	7	US-11-172-740-38	Sequence 38, Appl	665	29	36.7	689	7	US-11-087-099-911	Sequence 911, App
593	29	36.7	393	7	US-11-188-298-10324	Sequence 10324, A	666	29	36.7	717	7	US-11-096-568A-33955	Sequence 33955, A
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595	29	36.7	395	7	US-11-188-298-10115	Sequence 10115, A	668	29	36.7	725	7	US-11-079-463-8952	Sequence 8952, App
596	29	36.7	396	7	US-11-096-568A-19736	Sequence 19736, A	669	29	36.7	740	7	US-11-079-463-8625	Sequence 8625, App
597	29	36.7	396	7	US-11-096-568A-31930	Sequence 31930, A	670	29	36.7	762	6	US-10-330-773-898	Sequence 898, App
598	29	36.7	397	7	US-11-096-568A-2988	Sequence 2988, App	671	29	36.7	763	7	US-11-188-298-13343	Sequence 13343, A
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603	29	36.7	407	7	US-11-188-298-464	Sequence 464, App	676	29	36.7	842	7	US-11-045-004-2517	Sequence 2517, App
604	29	36.7	409	7	US-11-219-282-33	Sequence 33, Appl	677	29	36.7	856	7	US-11-079-463-5325	Sequence 5325, App
605	29	36.7	409	7	US-11-096-568A-19735	Sequence 19735, A	678	29	36.7	865	7	US-11-087-099-1496	Sequence 1496, App
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607	29	36.7	409	7	US-11-188-298-15630	Sequence 15630, A	680	29	36.7	916	6	US-10-467-657-5232	Sequence 5232, App
608	29	36.7	411	6	US-10-467-657-5868	Sequence 5868, App	681	29	36.7	921	6	US-10-467-657-7354	Sequence 7354, App
609	29	36.7	415	7	US-11-087-099-1187	Sequence 1187, App	682	29	36.7	929	7	US-11-087-099-6648	Sequence 6648, App

683	29	36.7	929	7	US-11-087-099-7898	Sequence 7898, Ap	756	28	35.4	176	7	US-11-096-568A-7838	Sequence 7838, Ap
684	29	36.7	940	7	US-11-079-463-9509	Sequence 9509, Ap	757	28	35.4	180	7	US-11-072-512-3862	Sequence 3862, Ap
685	29	36.7	954	7	US-11-096-568A-31293	Sequence 31293, A	758	28	35.4	183	7	US-11-045-004-820	Sequence 820, App
686	29	36.7	963	6	US-10-467-9628-2	Sequence 2, Appli	759	28	35.4	189	6	US-10-873-528-15	Sequence 15, Appl
687	29	36.7	963	7	US-11-096-568A-31292	Sequence 31292, A	760	28	35.4	189	6	US-11-096-568A-3488	Sequence 3488, Ap
688	29	36.7	964	7	US-11-096-568A-31291	Sequence 31291, A	761	28	35.4	189	7	US-11-098-686-10528	Sequence 10528, A
689	29	36.7	1031	6	US-10-857-780-22	Sequence 22, Appl	762	28	35.4	190	7	US-11-087-099-10323	Sequence 10323, A
690	29	36.7	1114	6	US-10-857-780-27	Sequence 27, Appl	763	28	35.4	193	6	US-10-537-897-33	Sequence 33, Appl
691	29	36.7	1160	7	US-11-188-298-19329	Sequence 19329, A	764	28	35.4	199	7	US-11-045-004-209	Sequence 209, App
692	29	36.7	1274	6	US-10-454-437-360	Sequence 360, App	765	28	35.4	204	6	US-10-467-657-8687	Sequence 8687, Ap
693	29	36.7	1331	7	US-11-096-568A-33412	Sequence 33412, A	766	28	35.4	207	7	US-11-096-568A-5969	Sequence 5969, Ap
694	29	36.7	1367	6	US-10-995-561-538	Sequence 538, App	767	28	35.4	209	7	US-11-188-298-4191	Sequence 4191, Ap
695	29	36.7	1367	6	US-10-510-903-10	Sequence 10, Appl	768	28	35.4	214	6	US-10-793-626-3124	Sequence 3124, Ap
696	29	36.7	1367	6	US-11-113-202-18	Sequence 18, Appl	769	28	35.4	216	7	US-11-096-568A-15125	Sequence 15125, A
697	29	36.7	1368	6	US-10-995-561-539	Sequence 539, App	770	28	35.4	218	7	US-11-096-568A-7822	Sequence 7822, Ap
698	29	36.7	1394	7	US-11-096-568A-33411	Sequence 33411, A	771	28	35.4	221	6	US-10-921-286B-18	Sequence 18, Appl
699	29	36.7	1482	7	US-11-096-568A-33410	Sequence 33410, A	772	28	35.4	221	6	US-10-921-286B-18	Sequence 18, Appl
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701	28.5	36.1	175	7	US-11-119-769-4	Sequence 4, Appli	774	28	35.4	221	7	US-11-188-298-11533	Sequence 11533, A
702	28.5	36.1	207	7	US-11-096-568A-10637	Sequence 10637, A	775	28	35.4	227	7	US-11-096-568A-17049	Sequence 17049, A
703	28.5	36.1	226	6	US-11-096-568A-10636	Sequence 10636, A	776	28	35.4	227	7	US-11-188-298-6867	Sequence 6867, Ap
704	28.5	36.1	320	6	US-10-965-103-36	Sequence 36, Appl	777	28	35.4	227	7	US-11-188-298-13693	Sequence 13693, A
705	28.5	36.1	442	7	US-11-087-099-1764	Sequence 1764, Ap	778	28	35.4	227	7	US-11-188-298-20592	Sequence 20592, A
706	28.5	36.1	442	7	US-11-188-298-1756	Sequence 1756, Ap	779	28	35.4	228	7	US-11-104-111-8	Sequence 8, Appli
707	28.5	36.1	487	6	US-10-131-826A-528	Sequence 528, App	780	28	35.4	228	7	US-11-188-298-1688	Sequence 1688, Ap
708	28.5	36.1	487	6	US-10-973-115B-528	Sequence 528, App	781	28	35.4	228	7	US-11-188-298-21739	Sequence 21739, A
709	28.5	36.1	487	6	US-10-213-535-18	Sequence 18, Appl	782	28	35.4	229	6	US-10-923-327-14	Sequence 14, Appl
710	28.5	36.1	487	6	US-10-218-784-204	Sequence 204, App	783	28	35.4	231	7	US-11-072-512-3576	Sequence 3576, Ap
711	28.5	36.1	487	6	US-10-219-061-204	Sequence 204, App	784	28	35.4	231	7	US-11-188-298-19681	Sequence 19681, A
712	28.5	36.1	487	6	US-10-219-062-204	Sequence 204, App	785	28	35.4	233	6	US-10-923-327-19	Sequence 19, Appl
713	28.5	36.1	487	6	US-10-219-064-204	Sequence 204, App	786	28	35.4	233	7	US-11-072-512-3056	Sequence 3056, Ap
714	28.5	36.1	487	6	US-10-233-134-204	Sequence 204, App	787	28	35.4	233	7	US-11-096-568A-15123	Sequence 15123, A
715	28.5	36.1	487	7	US-11-290-153-528	Sequence 528, App	788	28	35.4	237	7	US-11-188-298-3529	Sequence 3529, Ap
716	28.5	36.1	487	7	US-11-288-493-16	Sequence 16, Appl	789	28	35.4	237	7	US-11-188-298-16928	Sequence 16928, A
717	28.5	36.1	651	7	US-11-194-246-342	Sequence 342, App	790	28	35.4	237	7	US-11-045-004-1993	Sequence 1993, Ap
718	28.5	36.1	715	7	US-11-072-512-3385	Sequence 3385, Ap	791	28	35.4	238	7	US-11-096-568A-16506	Sequence 16506, A
719	28.5	36.1	748	7	US-11-090-617-692	Sequence 692, App	792	28	35.4	239	6	US-10-793-626-3010	Sequence 3010, Ap
720	28.5	36.1	781	7	US-11-072-512-2937	Sequence 2937, Ap	793	28	35.4	240	6	US-10-503-939-33	Sequence 33, Appl
721	28.5	36.1	796	7	US-11-188-298-3033	Sequence 3033, Ap	794	28	35.4	240	6	US-10-503-939-34	Sequence 34, Appl
722	28.5	36.1	798	7	US-11-188-298-10633	Sequence 10633, A	795	28	35.4	240	6	US-10-503-939-35	Sequence 35, Appl
723	28.5	36.1	1032	7	US-11-079-463-7811	Sequence 7811, Ap	796	28	35.4	240	6	US-10-503-939-36	Sequence 36, Appl
724	28.5	36.1	1039	6	US-10-915-002-321	Sequence 321, App	797	28	35.4	240	6	US-10-503-939-37	Sequence 37, Appl
725	28.5	36.1	1039	6	US-10-915-002-322	Sequence 322, App	798	28	35.4	240	6	US-10-503-939-38	Sequence 38, Appl
726	28.5	36.1	1039	6	US-10-915-002-323	Sequence 323, App	799	28	35.4	240	6	US-10-503-939-39	Sequence 39, Appl
727	28	35.4	34	6	US-11-004-399-2237	Sequence 2237, Ap	800	28	35.4	240	6	US-10-503-939-40	Sequence 40, Appl
728	28	35.4	46	6	US-10-467-657-8850	Sequence 8850, Ap	801	28	35.4	240	6	US-10-503-939-41	Sequence 41, Appl
729	28	35.4	52	6	US-10-914-165-34	Sequence 34, Appl	802	28	35.4	240	7	US-11-087-099-535	Sequence 535, App
730	28	35.4	79	7	US-11-112-784-3	Sequence 3, Appli	803	28	35.4	240	7	US-11-188-298-596	Sequence 596, App
731	28	35.4	86	7	US-11-112-784-2	Sequence 2, Appli	804	28	35.4	242	7	US-11-096-568A-3051	Sequence 3051, Ap
732	28	35.4	89	7	US-11-188-298-3147	Sequence 3147, Ap	805	28	35.4	245	7	US-11-183-664-13	Sequence 13, Appl
733	28	35.4	91	7	US-11-045-004-2772	Sequence 2772, Ap	806	28	35.4	245	7	US-11-188-298-5517	Sequence 5517, Ap
734	28	35.4	101	6	US-10-467-657-5070	Sequence 5070, Ap	807	28	35.4	245	7	US-11-188-298-14482	Sequence 14482, A
735	28	35.4	111	6	US-10-793-626-384	Sequence 384, App	808	28	35.4	246	7	US-11-087-099-1559	Sequence 1559, Ap
736	28	35.4	114	6	US-10-923-327-4	Sequence 4, Appli	809	28	35.4	246	7	US-11-188-298-4441	Sequence 4441, Ap
737	28	35.4	121	6	US-10-703-799B-116	Sequence 116, App	810	28	35.4	246	7	US-11-188-298-9052	Sequence 9052, Ap
738	28	35.4	121	6	US-11-208-422-52	Sequence 52, Appl	811	28	35.4	246	7	US-11-188-298-12483	Sequence 12483, A
739	28	35.4	122	6	US-10-067-974-14	Sequence 14, Appl	812	28	35.4	246	7	US-11-188-298-14962	Sequence 14962, A
740	28	35.4	122	6	US-10-793-626-2764	Sequence 2764, Ap	813	28	35.4	246	7	US-11-188-298-22352	Sequence 22352, A
741	28	35.4	123	7	US-11-087-099-414	Sequence 414, App	814	28	35.4	247	6	US-10-503-939-1	Sequence 1, Appli
742	28	35.4	127	6	US-10-530-104-14	Sequence 14, Appl	815	28	35.4	247	6	US-10-503-939-3	Sequence 3, Appli
743	28	35.4	129	6	US-11-045-004-1781	Sequence 1781, Ap	816	28	35.4	247	6	US-10-503-939-5	Sequence 5, Appli
744	28	35.4	133	6	US-11-246-980-2	Sequence 2, Appli	817	28	35.4	247	6	US-10-503-939-7	Sequence 7, Appli
745	28	35.4	138	6	US-10-793-626-1540	Sequence 1540, Ap	818	28	35.4	247	6	US-10-503-939-8	Sequence 8, Appli
746	28	35.4	145	6	US-10-793-626-2328	Sequence 2328, Ap	819	28	35.4	247	6	US-10-503-939-9	Sequence 9, Appli
747	28	35.4	149	6	US-10-995-561-763	Sequence 763, App	820	28	35.4	247	6	US-10-503-939-10	Sequence 10, Appl
748	28	35.4	150	7	US-11-123-241-70	Sequence 70, Appl	821	28	35.4	247	6	US-10-503-939-11	Sequence 11, Appl
749	28	35.4	151	7	US-11-045-004-1609	Sequence 1609, Ap	822	28	35.4	247	6	US-10-503-939-12	Sequence 12, Appl
750	28	35.4	153	6	US-10-793-626-1838	Sequence 1838, Ap	823	28	35.4	247	6	US-10-503-939-13	Sequence 13, Appl
751	28	35.4	162	7	US-11-096-568A-9446	Sequence 9446, Ap	824	28	35.4	248	6	US-10-923-327-16	Sequence 16, Appl
752	28	35.4	170	7	US-11-087-099-8302	Sequence 8302, Ap	825	28	35.4	248	7	US-11-156-516-36	Sequence 36, Appl
753	28	35.4	175	7	US-11-096-568A-842	Sequence 842, App	826	28	35.4	249	7	US-11-096-568A-14605	Sequence 14605, A
754	28	35.4	176	6	US-10-793-626-612	Sequence 612, App	827	28	35.4	250	6	US-10-067-974-10	Sequence 10, Appl
755	28	35.4	176	7	US-11-087-099-1975	Sequence 1975, Ap	828	28	35.4	250	6	US-10-503-939-24	Sequence 24, Appl

829	28	35.4	250	6	US-10-503-939-25	Sequence 25, Appl	902	28	35.4	327	7	US-11-087-099-10008	Sequence 10008, A
830	28	35.4	250	6	US-10-503-939-26	Sequence 26, Appl	903	28	35.4	328	7	US-11-096-568A-13515	Sequence 13515, A
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832	28	35.4	250	6	US-10-503-939-28	Sequence 28, Appl	905	28	35.4	330	6	US-10-330-773-45	Sequence 45, Appl
833	28	35.4	250	6	US-10-503-939-29	Sequence 29, Appl	906	28	35.4	330	6	US-11-087-099-5512	Sequence 5512, Ap
834	28	35.4	250	6	US-10-503-939-30	Sequence 30, Appl	907	28	35.4	333	6	US-10-793-626-2890	Sequence 2890, Ap
835	28	35.4	250	6	US-10-503-939-31	Sequence 31, Appl	908	28	35.4	334	7	US-11-087-099-4055	Sequence 4055, Ap
836	28	35.4	250	6	US-10-503-939-32	Sequence 32, Appl	909	28	35.4	334	7	US-11-188-298-14740	Sequence 14740, A
837	28	35.4	250	6	US-10-503-939-33	Sequence 33, Appl	910	28	35.4	334	7	US-11-096-568A-7553	Sequence 7553, Ap
838	28	35.4	250	6	US-10-507-720-45	Sequence 45, Appl	911	28	35.4	336	6	US-10-995-793-2	Sequence 2, Appl
839	28	35.4	250	7	US-11-045-004-2451	Sequence 48, Appl	912	28	35.4	337	7	US-11-087-099-4824	Sequence 4824, Ap
840	28	35.4	251	7	US-11-096-568A-7120	Sequence 7120, Ap	913	28	35.4	339	7	US-11-079-463-9761	Sequence 9761, Ap
841	28	35.4	251	7	US-11-172-740-1881	Sequence 1881, Ap	914	28	35.4	343	7	US-11-087-099-9113	Sequence 9113, Ap
842	28	35.4	256	7	US-11-096-568A-3050	Sequence 3050, Ap	915	28	35.4	343	7	US-11-096-568A-31752	Sequence 31752, A
843	28	35.4	256	7	US-11-096-568A-3052	Sequence 3052, Ap	916	28	35.4	343	7	US-11-079-463-7042	Sequence 7042, Ap
844	28	35.4	259	7	US-11-096-568A-31754	Sequence 31754, A	917	28	35.4	343	7	US-11-188-298-9040	Sequence 9040, Ap
845	28	35.4	261	7	US-11-096-568A-17990	Sequence 17990, A	918	28	35.4	344	6	US-10-453-372-190	Sequence 190, App
846	28	35.4	265	7	US-11-096-568A-16505	Sequence 16505, A	919	28	35.4	346	7	US-11-079-463-7987	Sequence 7987, Ap
847	28	35.4	267	6	US-10-503-939-15	Sequence 15, Appl	920	28	35.4	347	7	US-11-188-298-6375	Sequence 6375, Ap
848	28	35.4	267	6	US-10-503-939-16	Sequence 16, Appl	921	28	35.4	352	7	US-11-172-740-117	Sequence 117, App
849	28	35.4	267	6	US-10-503-939-17	Sequence 17, Appl	922	28	35.4	354	7	US-11-096-568A-13514	Sequence 13514, A
850	28	35.4	267	6	US-10-503-939-18	Sequence 18, Appl	923	28	35.4	354	7	US-11-188-298-15654	Sequence 15654, A
851	28	35.4	267	6	US-10-503-939-19	Sequence 19, Appl	924	28	35.4	355	7	US-11-096-568A-15348	Sequence 15348, A
852	28	35.4	267	6	US-10-503-939-20	Sequence 20, Appl	925	28	35.4	358	7	US-11-188-298-15146	Sequence 15146, A
853	28	35.4	267	6	US-10-503-939-21	Sequence 21, Appl	926	28	35.4	359	7	US-11-087-099-12362	Sequence 12362, A
854	28	35.4	267	6	US-10-503-939-22	Sequence 22, Appl	927	28	35.4	359	7	US-11-096-568A-17048	Sequence 17048, A
855	28	35.4	267	6	US-10-503-939-23	Sequence 23, Appl	928	28	35.4	360	6	US-10-467-657-5722	Sequence 5722, Ap
856	28	35.4	269	7	US-11-072-512-3593	Sequence 3593, Ap	929	28	35.4	360	7	US-11-096-568A-7552	Sequence 7552, A
857	28	35.4	281	7	US-11-096-568A-7119	Sequence 7119, Ap	930	28	35.4	360	7	US-11-188-298-19142	Sequence 19142, Ap
858	28	35.4	275	7	US-11-087-099-2636	Sequence 2636, Ap	931	28	35.4	363	7	US-11-188-298-20789	Sequence 20789, A
859	28	35.4	275	7	US-11-246-980-25	Sequence 25, Appl	932	28	35.4	364	7	US-11-096-568A-7820	Sequence 7820, Ap
860	28	35.4	277	7	US-11-096-568A-5921	Sequence 5921, Ap	933	28	35.4	366	6	US-10-524-647-126	Sequence 126, App
861	28	35.4	280	7	US-11-096-568A-5968	Sequence 5968, Ap	934	28	35.4	366	6	US-10-524-972-114	Sequence 114, App
862	28	35.4	281	7	US-11-096-568A-5920	Sequence 5920, Ap	935	28	35.4	366	7	US-11-087-099-4133	Sequence 4133, Ap
863	28	35.4	284	6	US-10-510-386-72	Sequence 72, Appl	936	28	35.4	367	6	US-11-087-099-2059	Sequence 2059, Ap
864	28	35.4	284	7	US-11-087-099-966	Sequence 966, App	937	28	35.4	369	6	US-10-515-547-2	Sequence 2, Appl
865	28	35.4	286	7	US-11-096-568A-5919	Sequence 5919, Ap	938	28	35.4	370	7	US-11-096-568A-2975	Sequence 2975, Ap
866	28	35.4	286	7	US-11-172-740-776	Sequence 776, App	939	28	35.4	370	7	US-11-096-568A-2977	Sequence 2977, Ap
867	28	35.4	287	7	US-11-188-298-356	Sequence 356, App	940	28	35.4	371	7	US-11-172-740-777	Sequence 777, App
868	28	35.4	289	7	US-11-194-246-291	Sequence 291, App	941	28	35.4	372	6	US-10-793-626-1632	Sequence 1632, Ap
869	28	35.4	289	7	US-11-188-298-3378	Sequence 3378, Ap	942	28	35.4	374	6	US-10-520-820-4	Sequence 4, Appl
870	28	35.4	292	7	US-11-096-568A-13516	Sequence 13516, A	943	28	35.4	375	7	US-11-172-740-778	Sequence 778, App
871	28	35.4	296	7	US-11-098-686-10566	Sequence 10566, A	944	28	35.4	379	7	US-11-045-004-2049	Sequence 2049, Ap
872	28	35.4	296	7	US-11-246-980-27	Sequence 27, Appl	945	28	35.4	385	7	US-11-087-099-2502	Sequence 2502, Ap
873	28	35.4	296	7	US-11-079-463-6624	Sequence 6624, Ap	946	28	35.4	385	7	US-11-188-298-2578	Sequence 2578, Ap
874	28	35.4	299	7	US-11-079-463-9990	Sequence 9990, Ap	947	28	35.4	386	7	US-11-288-493-60	Sequence 60, Appl
875	28	35.4	300	7	US-11-165-226-130	Sequence 130, App	948	28	35.4	387	7	US-11-096-568A-31216	Sequence 31216, A
876	28	35.4	301	7	US-11-087-099-434	Sequence 434, App	949	28	35.4	389	7	US-11-096-568A-2974	Sequence 2974, A
877	28	35.4	301	7	US-11-096-568A-10888	Sequence 10888, A	950	28	35.4	391	7	US-11-087-099-1565	Sequence 1565, Ap
878	28	35.4	302	7	US-11-079-463-8516	Sequence 8516, Ap	951	28	35.4	394	7	US-11-096-568A-31215	Sequence 31215, A
879	28	35.4	303	7	US-11-079-463-7767	Sequence 7767, Ap	952	28	35.4	394	7	US-11-096-568A-17047	Sequence 17047, A
880	28	35.4	304	7	US-11-153-238-2	Sequence 2, Appl	953	28	35.4	399	7	US-11-096-568A-26467	Sequence 26467, A
881	28	35.4	304	7	US-11-096-568A-7821	Sequence 7821, Ap	954	28	35.4	399	7	US-11-188-298-15324	Sequence 15324, A
882	28	35.4	304	7	US-11-188-298-20481	Sequence 20481, A	955	28	35.4	399	7	US-11-045-004-21	Sequence 21, Appl
883	28	35.4	305	7	US-11-087-099-1036	Sequence 1036, Ap	956	28	35.4	400	7	US-11-079-463-9030	Sequence 9030, Ap
884	28	35.4	306	7	US-11-045-004-76	Sequence 76, Appl	957	28	35.4	405	6	US-11-188-298-9056	Sequence 9056, Ap
885	28	35.4	309	7	US-11-096-568A-5967	Sequence 5967, Ap	958	28	35.4	406	6	US-10-453-372-188	Sequence 188, App
886	28	35.4	314	6	US-10-995-793-73	Sequence 73, Appl	959	28	35.4	409	6	US-10-793-626-2002	Sequence 2002, Ap
887	28	35.4	314	7	US-11-087-099-5586	Sequence 5586, Ap	960	28	35.4	409	6	US-10-793-626-2306	Sequence 2306, Ap
888	28	35.4	314	7	US-11-096-568A-31753	Sequence 31753, A	961	28	35.4	412	7	US-11-188-298-2343	Sequence 2343, Ap
889	28	35.4	314	7	US-11-079-463-5833	Sequence 5833, Ap	962	28	35.4	412	7	US-11-188-298-3285	Sequence 3285, Ap
890	28	35.4	317	7	US-11-112-784-6	Sequence 6, Appl	963	28	35.4	412	7	US-11-188-298-10609	Sequence 10609, A
891	28	35.4	317	7	US-11-112-784-5	Sequence 5, Appl	964	28	35.4	414	7	US-11-188-298-13961	Sequence 13961, A
892	28	35.4	317	7	US-11-112-784-7	Sequence 7, Appl	965	28	35.4	419	7	US-11-188-298-22443	Sequence 22443, A
893	28	35.4	317	7	US-11-112-784-8	Sequence 8, Appl	966	28	35.4	422	6	US-10-467-657-212	Sequence 212, App
894	28	35.4	317	7	US-11-087-099-2380	Sequence 2380, Ap	967	28	35.4	422	6	US-10-467-657-6516	Sequence 6516, Ap
895	28	35.4	317	7	US-11-087-099-6120	Sequence 6120, Ap	968	28	35.4	422	6	US-11-079-463-5965	Sequence 5965, Ap
896	28	35.4	317	7	US-11-096-568A-7837	Sequence 7837, Ap	969	28	35.4	422	7	US-11-188-298-19415	Sequence 19415, A
897	28	35.4	318	7	US-11-096-568A-250	Sequence 250, App	970	28	35.4	422	6	US-11-188-298-10609	Sequence 10609, A
898	28	35.4	322	6	US-10-501-035-332	Sequence 332, App	971	28	35.4	424	6	US-10-485-517-405	Sequence 405, App
899	28	35.4	322	7	US-11-096-568A-7836	Sequence 7836, App	972	28	35.4	425	6	US-10-793-626-1012	Sequence 1012, Ap
900	28	35.4	326	7	US-11-096-568A-3049	Sequence 3049, Ap	973	28	35.4	425	6	US-10-793-626-2434	Sequence 2434, Ap
901	28	35.4	326	7	US-11-096-568A-15349	Sequence 15349, A	974	28	35.4	438	7	US-11-096-568A-16134	Sequence 16134, A

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975 28 35.4 439 7 US-11-096-568A-26466 Sequence 26466, A
976 28 35.4 444 7 US-11-074-176-170 Sequence 170, App
977 28 35.4 448 7 US-11-196-710-9 Sequence 9, Appli
978 28 35.4 451 6 US-10-923-327-11 Sequence 11, Appl
979 28 35.4 451 7 US-11-208-422-22 Sequence 22, Appl
980 28 35.4 454 6 US-10-501-033-306 Sequence 306, App
981 28 35.4 454 7 US-11-196-710-5 Sequence 5, Appli
982 28 35.4 461 7 US-11-072-512-2367 Sequence 2367, Ap
983 28 35.4 461 7 US-11-087-099-5294 Sequence 5294, Ap
984 28 35.4 462 7 US-11-096-568A-1436 Sequence 1436, Ap
985 28 35.4 466 6 US-10-063-703-104 Sequence 104, App
986 28 35.4 466 6 US-10-194-487-316 Sequence 316, App
987 28 35.4 466 6 US-10-195-883-316 Sequence 316, App
988 28 35.4 466 6 US-10-195-888-316 Sequence 316, App
989 28 35.4 466 6 US-10-195-889-316 Sequence 316, App
990 28 35.4 466 7 US-11-102-240-104 Sequence 104, App
991 28 35.4 466 7 US-11-103-195-104 Sequence 104, App
992 28 35.4 466 7 US-11-072-512-366A Sequence 366A, App
993 28 35.4 470 7 US-11-087-099-12133 Sequence 12133, A
994 28 35.4 470 7 US-11-188-298-22260 Sequence 22260, A
995 28 35.4 474 7 US-11-087-099-11265 Sequence 11265, A
996 28 35.4 474 7 US-11-188-298-21394 Sequence 21394, A
997 28 35.4 475 7 US-11-153-238-1 Sequence 1, Appli
998 28 35.4 480 7 US-11-096-568A-249 Sequence 249, App
999 28 35.4 480 7 US-11-096-568A-251 Sequence 251, App
1000 28 35.4 481 7 US-11-072-512-3799 Sequence 3799, Ap
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ALIGNMENTS

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RESULT 1
US-11-124-368A-214
; Sequence 214, Application US/11124368A
; Publication No. US20050287559A1
; GENERAL INFORMATION:
; APPLICANT: Michele Cargill
; APPLICANT: James J. Devlin
; APPLICANT: May Luke
; TITLE OF INVENTION: Genetic Polymorphisms Associated with
; TITLE OF INVENTION: Vascular Diseases, Methods of Detection and Uses Thereof
; FILE REFERENCE: CL001524
; CURRENT APPLICATION NUMBER: US/11/124,368A
; CURRENT FILING DATE: 2005-05-09
; PRIOR APPLICATION NUMBER: US 60/568,845
; PRIOR FILING DATE: 2004-05-07
; PRIOR APPLICATION NUMBER: US 60/625,936
; PRIOR FILING DATE: 2004-11-09
; NUMBER OF SEQ ID NOS: 21112
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 214
; LENGTH: 2665
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-124-368A-214
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Query Match 100.0%; Score 79; DB 7; Length 2665;
Best Local Similarity 100.0%; Pred. No. 1.1e-05;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Qy 1 RHYGETKNQRRSSRS 15
| | | | | | | | | | | | | | | |
Db 189 RHYGETKNQRRSSRS 203
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RESULT 2
US-11-124-368A-215
; Sequence 215, Application US/11124368A
; Publication No. US20050287559A1
; GENERAL INFORMATION:
; APPLICANT: Michele Cargill
; APPLICANT: James J. Devlin
; APPLICANT: May Luke
```

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; TITLE OF INVENTION: Genetic Polymorphisms Associated with
; TITLE OF INVENTION: Vascular Diseases, Methods of Detection and Uses Thereof
; FILE REFERENCE: CL001524
; CURRENT APPLICATION NUMBER: US/11/124,368A
; CURRENT FILING DATE: 2005-05-09
; PRIOR APPLICATION NUMBER: US 60/568,845
; PRIOR FILING DATE: 2004-05-07
; PRIOR APPLICATION NUMBER: US 60/625,936
; PRIOR FILING DATE: 2004-11-09
; NUMBER OF SEQ ID NOS: 21112
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 215
; LENGTH: 2668
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-124-368A-215
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Query Match 100.0%; Score 79; DB 7; Length 2668;
Best Local Similarity 100.0%; Pred. No. 1.1e-05;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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```
Qy 1 RHYGETKNQRRSSRS 15
| | | | | | | | | | | | | | | |
Db 189 RHYGETKNQRRSSRS 203
```

```
RESULT 3
US-11-096-568A-32400
; Sequence 32400, Application US/11096568A
; Publication No. US20060048240A1
; GENERAL INFORMATION:
; APPLICANT: Alexandrov, Nickolai et al.
; TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
; FILE REFERENCE: 2750-1592PUS2
; CURRENT APPLICATION NUMBER: US/11/096,568A
; CURRENT FILING DATE: 2005-04-01
; NUMBER OF SEQ ID NOS: 34471
; SEQ ID NO 32400
; LENGTH: 726
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)..(726)
; OTHER INFORMATION: Ceres Seq. ID no. 13592891
US-11-096-568A-32400
```

```
Query Match 64.6%; Score 51; DB 7; Length 726;
Best Local Similarity 66.7%; Pred. No. 0.32;
Matches 10; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
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```
Qy 1 RHYGETKNQRRSSRS 15
| | | | | : | | | | |
Db 106 RKIGETSLNRSRS 120
```

```
RESULT 4
US-11-096-568A-28686
; Sequence 28686, Application US/11096568A
; Publication No. US20060048240A1
; GENERAL INFORMATION:
; APPLICANT: Alexandrov, Nickolai et al.
; TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
; FILE REFERENCE: 2750-1592PUS2
; CURRENT APPLICATION NUMBER: US/11/096,568A
; CURRENT FILING DATE: 2005-04-01
; NUMBER OF SEQ ID NOS: 34471
; SEQ ID NO 28686
; LENGTH: 743
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
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; FEATURE:
; NAME/KEY: misc.feature
; LOCATION: (1)..(743)
US-11-096-568A-28686

Query Match 64.6%; Score 51; DB 7; Length 743;
Best Local Similarity 66.7%; Pred. No. 0.33;
Matches 10; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 1 RHYGETKNQRSRS 15
| | | | | : | : | | | | |
Db 86 RKIGETSLNRSRS 100

RESULT 5

US-11-096-568A-32399
; Sequence 32399, Application US/11096568A
; Publication No. US20060048240A1
; GENERAL INFORMATION:
; APPLICANT: Alexandrov, Nikolai et al.
; TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
; FILE REFERENCE: 2750-1592PUS2
; CURRENT APPLICATION NUMBER: US/11/096,568A
; CURRENT FILING DATE: 2005-04-01
; NUMBER OF SEQ ID NOS: 34471
; SEQ ID NO 32399
; LENGTH: 829
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
; FEATURE:
; NAME/KEY: misc.feature
; LOCATION: (1)..(829)
; OTHER INFORMATION: Ceres Seq. ID no. 13592890
US-11-096-568A-32399

Query Match 64.6%; Score 51; DB 7; Length 829;
Best Local Similarity 66.7%; Pred. No. 0.37;
Matches 10; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 1 RHYGETKNQRSRS 15
| | | | | : | : | | | | |
Db 209 RKIGETSLNRSRS 223

RESULT 6

US-11-096-568A-32398
; Sequence 32398, Application US/11096568A
; Publication No. US20060048240A1
; GENERAL INFORMATION:
; APPLICANT: Alexandrov, Nikolai et al.
; TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
; FILE REFERENCE: 2750-1592PUS2
; CURRENT APPLICATION NUMBER: US/11/096,568A
; CURRENT FILING DATE: 2005-04-01
; NUMBER OF SEQ ID NOS: 34471
; SEQ ID NO 32398
; LENGTH: 834
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
; FEATURE:
; NAME/KEY: misc.feature
; LOCATION: (1)..(834)
; OTHER INFORMATION: Ceres Seq. ID no. 13592889
US-11-096-568A-32398

Query Match 64.6%; Score 51; DB 7; Length 834;
Best Local Similarity 66.7%; Pred. No. 0.37;
Matches 10; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 1 RHYGETKNQRSRS 15

Db 214 RKIGETSLNRSRS 228
| | | | | : | : | | | | |

RESULT 7

US-11-096-568A-28685
; Sequence 28685, Application US/11096568A
; Publication No. US20060048240A1
; GENERAL INFORMATION:
; APPLICANT: Alexandrov, Nikolai et al.
; TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
; FILE REFERENCE: 2750-1592PUS2
; CURRENT APPLICATION NUMBER: US/11/096,568A
; CURRENT FILING DATE: 2005-04-01
; NUMBER OF SEQ ID NOS: 34471
; SEQ ID NO 28685
; LENGTH: 851
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
; FEATURE:
; NAME/KEY: misc.feature
; LOCATION: (1)..(851)
; OTHER INFORMATION: Ceres Seq. ID no. 3036348
US-11-096-568A-28685

Query Match 64.6%; Score 51; DB 7; Length 851;
Best Local Similarity 66.7%; Pred. No. 0.38;
Matches 10; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 1 RHYGETKNQRSRS 15
| | | | | : | : | | | | |
Db 194 RKIGETSLNRSRS 208

RESULT 8

US-11-096-568A-28684
; Sequence 28684, Application US/11096568A
; Publication No. US20060048240A1
; GENERAL INFORMATION:
; APPLICANT: Alexandrov, Nikolai et al.
; TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
; FILE REFERENCE: 2750-1592PUS2
; CURRENT APPLICATION NUMBER: US/11/096,568A
; CURRENT FILING DATE: 2005-04-01
; NUMBER OF SEQ ID NOS: 34471
; SEQ ID NO 28684
; LENGTH: 862
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
; FEATURE:
; NAME/KEY: misc.feature
; LOCATION: (1)..(862)
; OTHER INFORMATION: Ceres Seq. ID no. 3036347
US-11-096-568A-28684

Query Match 64.6%; Score 51; DB 7; Length 862;
Best Local Similarity 66.7%; Pred. No. 0.38;
Matches 10; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 1 RHYGETKNQRSRS 15
| | | | | : | : | | | | |
Db 205 RKIGETSLNRSRS 219

RESULT 9

US-11-096-568A-29848
; Sequence 29848, Application US/11096568A
; Publication No. US20060048240A1
; GENERAL INFORMATION:
; APPLICANT: Alexandrov, Nikolai et al.
; TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides

```
; TITLE OF INVENTION: Therby
; FILE REFERENCE: 2750-1592PUS2
; CURRENT APPLICATION NUMBER: US/11/096,568A
; CURRENT FILING DATE: 2005-04-01
; NUMBER OF SEQ ID NOS: 34471
; SEQ ID NO 29846
; LENGTH: 811
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(811)
; OTHER INFORMATION: Ceres Seq. ID no. 4931842
US-11-096-568A-29848

Query Match      58.2%; Score 46; DB 7; Length 811;
Best Local Similarity 60.0%; Pred. No. 2.8;
Matches 9; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Qy      1 RHYGETKMQRSRS 15
Db      86 RQVGETALNDKSSRS 100

RESULT 10
US-11-096-568A-29847
; Sequence 29847, Application US/11096568A
; Publication No. US20060048240A1
; GENERAL INFORMATION:
; APPLICANT: Alexandrov, Nikolai et al.
; TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
; FILE REFERENCE: 2750-1592PUS2
; CURRENT APPLICATION NUMBER: US/11/096,568A
; CURRENT FILING DATE: 2005-04-01
; NUMBER OF SEQ ID NOS: 34471
; SEQ ID NO 29847
; LENGTH: 898
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(898)
; OTHER INFORMATION: Ceres Seq. ID no. 4931841
US-11-096-568A-29847

Query Match      58.2%; Score 46; DB 7; Length 898;
Best Local Similarity 60.0%; Pred. No. 3.2;
Matches 9; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Qy      1 RHYGETKMQRSRS 15
Db      173 RQVGETALNDKSSRS 187

RESULT 11
US-11-096-568A-29846
; Sequence 29846, Application US/11096568A
; Publication No. US20060048240A1
; GENERAL INFORMATION:
; APPLICANT: Alexandrov, Nikolai et al.
; TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
; FILE REFERENCE: 2750-1592PUS2
; CURRENT APPLICATION NUMBER: US/11/096,568A
; CURRENT FILING DATE: 2005-04-01
; NUMBER OF SEQ ID NOS: 34471
; SEQ ID NO 29846
; LENGTH: 932
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
; FEATURE:
; NAME/KEY: misc_feature
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```
; LOCATION: (1)..(932)
; OTHER INFORMATION: Ceres Seq. ID no. 4931840
US-11-096-568A-29846

Query Match      58.2%; Score 46; DB 7; Length 932;
Best Local Similarity 60.0%; Pred. No. 3.3;
Matches 9; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Qy      1 RHYGETKMQRSRS 15
Db      207 RQVGETALNDKSSRS 221

RESULT 12
US-11-045-004-555
; Sequence 555, Application US/11045004
; Publication No. US20060078901A1
; GENERAL INFORMATION:
; APPLICANT: BUCHRIESER, CARMEN
; APPLICANT: FRANGEUL, LIONEL
; APPLICANT: COUVE, ELISABETH
; APPLICANT: RUSNIOK, CHRISTOPHE
; APPLICANT: FSIHI, HAFIDA
; APPLICANT: DEHOUX, PIERRE
; APPLICANT: DUSSURGET, OLIVIER
; APPLICANT: CHETOUANI, FARID
; APPLICANT: NEDJARI, HAFED
; APPLICANT: GLASER, PHILIPPE
; APPLICANT: KUNST, FRANCK
; APPLICANT: COSSART, PASCALE
; APPLICANT: DANIELS, JUSTIN
; APPLICANT: GOBBEL, WERNER
; APPLICANT: KREFT, JURGEN
; APPLICANT: KUHN, MICHAEL
; APPLICANT: NG, EVA
; APPLICANT: VAZQUEZ-BOLAND, ANTONIO
; APPLICANT: DOMINGUEZ-BERNAL, GUSTAVO
; APPLICANT: GARRIDO-GARCIA, PATRICIA
; APPLICANT: TIERREZ-MARTINEZ, ALBERTO
; APPLICANT: AMEND, ALEXANDRA
; APPLICANT: CHAKRABORTY, TRINAD
; APPLICANT: DOMANN, EUGEN
; APPLICANT: HAIN, THORSTEN
; APPLICANT: BERCHE, PATRICK
; APPLICANT: CHARBIT, ALAIN
; APPLICANT: DURANT, LIONEL
; APPLICANT: PEREZ-DIAZ, JOSE-CLAUDIO
; APPLICANT: BAQUERO, FERNANDO
; APPLICANT: GARCIA DEL PORTILLO, FRANCISCO
; APPLICANT: GOMEZ-LOPEZ, NURIA
; APPLICANT: MADUENIO, ENCARNIA
; APPLICANT: PABLOS, BETRIZ DE
; APPLICANT: WEHLAND, JURGEN
; APPLICANT: KARST, UWE
; APPLICANT: ENTIAN, KARL-DIETER
; APPLICANT: HAUF, JORG
; APPLICANT: ROSE, MATTHIAS
; APPLICANT: VOSS, HAMUT
; TITLE OF INVENTION: LISTERIA MONOCYTOGENES GENOME, POLYPEPTIDES AND USES
; FILE REFERENCE: 05394.0018-02
; CURRENT APPLICATION NUMBER: US/11/045,004
; CURRENT FILING DATE: 2005-01-28
; PRIOR APPLICATION NUMBER: 10/637,657
; PRIOR FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: 10/257,023
; PRIOR FILING DATE: 2002-10-08
; PRIOR APPLICATION NUMBER: PCT/FR01/01118
; PRIOR FILING DATE: 2001-04-11
; PRIOR APPLICATION NUMBER: FR 00/04,629
; PRIOR FILING DATE: 2000-04-11
; NUMBER OF SEQ ID NOS: 2854
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 555
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; LENGTH: 315
; TYPE: PRT
; ORGANISM: Listeria monocytogenes
US-11-045-004-555

Query Match      57.0%; Score 45; DB 7; Length 315;
Best Local Similarity 75.0%; Pred. No. 1.6;
Matches 9; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      1 RHYGETKNQRS 12
      || ||| ||| |||
Db      201 RHAGETKNYRS 212

RESULT 13
US-11-051-720-1349
; Sequence 1349, Application US/11051720
; Publication No. US20060046257A1
; GENERAL INFORMATION:
; APPLICANT: Compugen Ltd
; TITLE OF INVENTION: NOVEL NUCLEOTIDE AND AMINO ACID SEQUENCES, AND ASSAYS AND METHODS
; FILE REFERENCE: 1847.1002
; CURRENT APPLICATION NUMBER: US/11/051,720
; CURRENT FILING DATE: 2005-01-27
; NUMBER OF SEQ ID NOS: 1780
; SEQ ID NO 1349
; LENGTH: 324
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-051-720-1349

Query Match      57.0%; Score 45; DB 7; Length 324;
Best Local Similarity 60.0%; Pred. No. 1.7;
Matches 9; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY      1 RHYGETKNQRSRS 15
      || ||| ||| |||
Db      191 RHVAVTNMNEHSRS 205

RESULT 14
US-11-051-720-1348
; Sequence 1348, Application US/11051720
; Publication No. US20060046257A1
; GENERAL INFORMATION:
; APPLICANT: Compugen Ltd
; TITLE OF INVENTION: NOVEL NUCLEOTIDE AND AMINO ACID SEQUENCES, AND ASSAYS AND METHODS
; FILE REFERENCE: 1847.1002
; CURRENT APPLICATION NUMBER: US/11/051,720
; CURRENT FILING DATE: 2005-01-27
; NUMBER OF SEQ ID NOS: 1780
; SEQ ID NO 1348
; LENGTH: 385
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-051-720-1348

Query Match      57.0%; Score 45; DB 7; Length 385;
Best Local Similarity 60.0%; Pred. No. 2;
Matches 9; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY      1 RHYGETKNQRSRS 15
      || ||| ||| |||
Db      191 RHVAVTNMNEHSRS 205

RESULT 15
US-11-051-720-1346
; Sequence 1346, Application US/11051720
; Publication No. US20060046257A1
; GENERAL INFORMATION:
; APPLICANT: Compugen Ltd
; TITLE OF INVENTION: NOVEL NUCLEOTIDE AND AMINO ACID SEQUENCES, AND ASSAYS AND METHODS
; FILE REFERENCE: 1847.1002
; CURRENT APPLICATION NUMBER: US/11/051,720
; CURRENT FILING DATE: 2005-01-27
; NUMBER OF SEQ ID NOS: 1780
; SEQ ID NO 1346
; LENGTH: 514
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-051-720-1346

Query Match      57.0%; Score 45; DB 7; Length 514;
Best Local Similarity 60.0%; Pred. No. 2.7;
Matches 9; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY      1 RHYGETKNQRSRS 15
      || ||| ||| |||
Db      191 RHVAVTNMNEHSRS 205

RESULT 16
US-11-051-720-1345
; Sequence 1345, Application US/11051720
; Publication No. US20060046257A1
; GENERAL INFORMATION:
; APPLICANT: Compugen Ltd
; TITLE OF INVENTION: NOVEL NUCLEOTIDE AND AMINO ACID SEQUENCES, AND ASSAYS AND METHODS
; FILE REFERENCE: 1847.1002
; CURRENT APPLICATION NUMBER: US/11/051,720
; CURRENT FILING DATE: 2005-01-27
; NUMBER OF SEQ ID NOS: 1780
; SEQ ID NO 1345
; LENGTH: 737
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-051-720-1345

Query Match      57.0%; Score 45; DB 7; Length 737;
Best Local Similarity 60.0%; Pred. No. 3.9;
Matches 9; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY      1 RHYGETKNQRSRS 15
      || ||| ||| |||
Db      191 RHVAVTNMNEHSRS 205

RESULT 17
US-10-330-773-712
; Sequence 712, Application US/10330773
; Publication No. US20060040262A1
; GENERAL INFORMATION:
; APPLICANT: David W. Morris
; APPLICANT: Marc Malandro
; TITLE OF INVENTION: Novel Compositions and Methods in Cancer
; FILE REFERENCE: 529452001300
; CURRENT APPLICATION NUMBER: US/10/330,773
; CURRENT FILING DATE: 2002-12-27
; NUMBER OF SEQ ID NOS: 981
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 712
; LENGTH: 911
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-330-773-712

Query Match      57.0%; Score 45; DB 6; Length 911;
Best Local Similarity 60.0%; Pred. No. 4.9;
Matches 9; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY      1 RHYGETKNQRSRS 15
```

Db 149 RHVAVTNNEHSRS 163
|| | ||: ||||

RESULT 18

US-10-330-773-709
; Sequence 709, Application US/10330773
; Publication No. US20060040262A1
; GENERAL INFORMATION:
; APPLICANT: David W. Morris
; APPLICANT: Marc Malandro
; TITLE OF INVENTION: Novel Compositions and Methods in Cancer
; FILE REFERENCE: 529452001300
; CURRENT APPLICATION NUMBER: US/10/330,773
; CURRENT FILING DATE: 2002-12-27
; NUMBER OF SEQ ID NOS: 981
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 709
; LENGTH: 952
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-330-773-709

Query Match 57.0%; Score 45; DB 6; Length 952;
Best Local Similarity 60.0%; Pred. No. 5.1;
Matches 9; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 1 RHYGETKNQSRSS 15
|| | ||: ||||
Db 191 RHVAVTNNEHSRS 205

RESULT 19

US-11-051-720-1438
; Sequence 1438, Application US/11051720
; Publication No. US20060046257A1
; GENERAL INFORMATION:
; APPLICANT: Compugen Ltd
; TITLE OF INVENTION: NOVEL NUCLEOTIDE AND AMINO ACID SEQUENCES, AND ASSAYS AND METHODS THEREOF FOR DIAGNOSIS OF LUNG CANCER
; FILE REFERENCE: 1847.1002
; CURRENT APPLICATION NUMBER: US/11/051,720
; CURRENT FILING DATE: 2005-01-27
; NUMBER OF SEQ ID NOS: 1780
; SEQ ID NO 1438
; LENGTH: 957
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-051-720-1438

Query Match 57.0%; Score 45; DB 7; Length 957;
Best Local Similarity 60.0%; Pred. No. 5.1;
Matches 9; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 1 RHYGETKNQSRSS 15
|| | ||: ||||
Db 191 RHVAVTNNEHSRS 205

RESULT 20

US-11-096-568A-26779
; Sequence 26779, Application US/11096568A
; Publication No. US20060048240A1
; GENERAL INFORMATION:
; APPLICANT: Alexandrov, Nikolai et al.
; TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
; FILE REFERENCE: 2750-1592FUS2
; CURRENT APPLICATION NUMBER: US/11/096,568A
; CURRENT FILING DATE: 2005-04-01
; NUMBER OF SEQ ID NOS: 34471
; SEQ ID NO 26779
; LENGTH: 292

; TYPE: PRT
; ORGANISM: Zea mays subsp. mays
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(292)
; OTHER INFORMATION: Ceres Seq. ID no. 13600527
US-11-096-568A-26779

Query Match 55.7%; Score 44; DB 7; Length 292;
Best Local Similarity 60.0%; Pred. No. 2.3;
Matches 9; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 RHYGETKNQSRSS 15
| | | : | | | |
Db 8 RAVGSTALNERSRS 22

RESULT 21

US-11-096-568A-26778
; Sequence 26778, Application US/11096568A
; Publication No. US20060048240A1
; GENERAL INFORMATION:
; APPLICANT: Alexandrov, Nikolai et al.
; TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
; FILE REFERENCE: 2750-1592FUS2
; CURRENT APPLICATION NUMBER: US/11/096,568A
; CURRENT FILING DATE: 2005-04-01
; NUMBER OF SEQ ID NOS: 34471
; SEQ ID NO 26778
; LENGTH: 331
; TYPE: PRT
; ORGANISM: Zea mays subsp. mays
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(331)
; OTHER INFORMATION: Ceres Seq. ID no. 13600526
US-11-096-568A-26778

Query Match 55.7%; Score 44; DB 7; Length 331;
Best Local Similarity 60.0%; Pred. No. 2.6;
Matches 9; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 RHYGETKNQSRSS 15
| | | : | | | |
Db 47 RAVGSTALNERSRS 61

RESULT 22

US-11-096-568A-26777
; Sequence 26777, Application US/11096568A
; Publication No. US20060048240A1
; GENERAL INFORMATION:
; APPLICANT: Alexandrov, Nikolai et al.
; TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
; FILE REFERENCE: 2750-1592FUS2
; CURRENT APPLICATION NUMBER: US/11/096,568A
; CURRENT FILING DATE: 2005-04-01
; NUMBER OF SEQ ID NOS: 34471
; SEQ ID NO 26777
; LENGTH: 338
; TYPE: PRT
; ORGANISM: Zea mays subsp. mays
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(338)
; OTHER INFORMATION: Ceres Seq. ID no. 13600525
US-11-096-568A-26777

Query Match 55.7%; Score 44; DB 7; Length 338;
Best Local Similarity 60.0%; Pred. No. 2.6;
Matches 9; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

```
; APPLICANT: Alexandrov, Nikolai et al.
; TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
; FILE REFERENCE: 2750-1592PUS2
; CURRENT APPLICATION NUMBER: US/11/096,568A
; CURRENT FILING DATE: 2005-04-01
; NUMBER OF SEQ ID NOS: 34471
; SEQ ID NO 26771
; LENGTH: 842
; TYPE: PRT
; ORGANISM: Zea mays subsp. mays
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(842)
; OTHER INFORMATION: Ceres Seq. ID no. 13600312
US-11-096-568A-26770

Query Match          55.7%; Score 44; DB 7; Length 842;
Best Local Similarity 60.0%; Pred. No. 6.8;
Matches 9; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 RHYGETKNQSRSS 15
| | | | |
Db 54 RAVGSTALNERS 68
| | | | |

RESULT 23
US-11-096-568A-26771
; Sequence 26771, Application US/11096568A
; Publication No. US20060048240A1
; GENERAL INFORMATION:
; APPLICANT: Alexandrov, Nikolai et al.
; TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
; FILE REFERENCE: 2750-1592PUS2
; CURRENT APPLICATION NUMBER: US/11/096,568A
; CURRENT FILING DATE: 2005-04-01
; NUMBER OF SEQ ID NOS: 34471
; SEQ ID NO 26771
; LENGTH: 799
; TYPE: PRT
; ORGANISM: Zea mays subsp. mays
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(799)
; OTHER INFORMATION: Ceres Seq. ID no. 13600313
US-11-096-568A-26771

Query Match          55.7%; Score 44; DB 7; Length 799;
Best Local Similarity 60.0%; Pred. No. 6.4;
Matches 9; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 RHYGETKNQSRSS 15
| | | | |
Db 470 RAVGSTALNERS 484
| | | | |

RESULT 24
US-11-096-568A-26949
; Sequence 26949, Application US/11096568A
; Publication No. US20060048240A1
; GENERAL INFORMATION:
; APPLICANT: Alexandrov, Nikolai et al.
; TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
; FILE REFERENCE: 2750-1592PUS2
; CURRENT APPLICATION NUMBER: US/11/096,568A
; CURRENT FILING DATE: 2005-04-01
; NUMBER OF SEQ ID NOS: 34471
; SEQ ID NO 26949
; LENGTH: 808
; TYPE: PRT
; ORGANISM: Zea mays subsp. mays
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(808)
; OTHER INFORMATION: Ceres Seq. ID no. 13635666
US-11-096-568A-26949

Query Match          55.7%; Score 44; DB 7; Length 808;
Best Local Similarity 60.0%; Pred. No. 6.5;
Matches 9; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 RHYGETKNQSRSS 15
| | | | |
Db 86 RRTGETYLNERS 100
| | | | |

RESULT 25
US-11-096-568A-26770
; Sequence 26770, Application US/11096568A
; Publication No. US20060048240A1
; GENERAL INFORMATION:
```

```
; APPLICANT: Alexandrov, Nikolai et al.
; TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
; FILE REFERENCE: 2750-1592PUS2
; CURRENT APPLICATION NUMBER: US/11/096,568A
; CURRENT FILING DATE: 2005-04-01
; NUMBER OF SEQ ID NOS: 34471
; SEQ ID NO 26770
; LENGTH: 842
; TYPE: PRT
; ORGANISM: Zea mays subsp. mays
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(842)
; OTHER INFORMATION: Ceres Seq. ID no. 13600312
US-11-096-568A-26770

Query Match          55.7%; Score 44; DB 7; Length 842;
Best Local Similarity 60.0%; Pred. No. 6.8;
Matches 9; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 RHYGETKNQSRSS 15
| | | | |
Db 513 RAVGSTALNERS 527
| | | | |

RESULT 26
US-11-096-568A-26769
; Sequence 26769, Application US/11096568A
; Publication No. US20060048240A1
; GENERAL INFORMATION:
; APPLICANT: Alexandrov, Nikolai et al.
; TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
; FILE REFERENCE: 2750-1592PUS2
; CURRENT APPLICATION NUMBER: US/11/096,568A
; CURRENT FILING DATE: 2005-04-01
; NUMBER OF SEQ ID NOS: 34471
; SEQ ID NO 26769
; LENGTH: 849
; TYPE: PRT
; ORGANISM: Zea mays subsp. mays
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(849)
; OTHER INFORMATION: Ceres Seq. ID no. 13600311
US-11-096-568A-26769

Query Match          55.7%; Score 44; DB 7; Length 849;
Best Local Similarity 60.0%; Pred. No. 6.8;
Matches 9; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 RHYGETKNQSRSS 15
| | | | |
Db 520 RAVGSTALNERS 534
| | | | |

RESULT 27
US-11-096-568A-26948
; Sequence 26948, Application US/11096568A
; Publication No. US20060048240A1
; GENERAL INFORMATION:
; APPLICANT: Alexandrov, Nikolai et al.
; TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
; FILE REFERENCE: 2750-1592PUS2
; CURRENT APPLICATION NUMBER: US/11/096,568A
; CURRENT FILING DATE: 2005-04-01
; NUMBER OF SEQ ID NOS: 34471
; SEQ ID NO 26948
; LENGTH: 897
; TYPE: PRT
; ORGANISM: Zea mays subsp. mays
```

;
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)..(897)
; OTHER INFORMATION: Ceres Seq. ID no. 13635665
US-11-096-568A-26948

Query Match 55.7%; Score 44; DB 7; Length 897;
Best Local Similarity 60.0%; Pred. No. 7.2;
Matches 9; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Qy 1 RHYGETKNQRRSSRS 15
| ||| :|: ||||
Db 175 RRTGETYLSNVSSRS 189

RESULT 28
US-11-096-568A-27943
; Sequence 27943, Application US/11096568A
; Publication No. US20060048240A1
; GENERAL INFORMATION:
; APPLICANT: Alexandrov, Nikolai et al.
; TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
; FILE REFERENCE: 2750-1592PUS2
; CURRENT APPLICATION NUMBER: US/11/096,568A
; CURRENT FILING DATE: 2005-04-01
; NUMBER OF SEQ ID NOS: 34471
; SEQ ID NO 27943
; LENGTH: 975
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
; NAME/KEY: misc feature
; LOCATION: (1)..(975)
; OTHER INFORMATION: Ceres Seq. ID no. 2142331
US-11-096-568A-27943

Query Match 54.4%; Score 43; DB 7; Length 975;
Best Local Similarity 60.0%; Pred. No. 12;
Matches 9; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Qy 1 RHYGETKNQRRSSRS 15
| ||| :|: ||||
Db 78 RKIGETSLNEVSSRS 92

RESULT 29
US-11-096-568A-27942
; Sequence 27942, Application US/11096568A
; Publication No. US20060048240A1
; GENERAL INFORMATION:
; APPLICANT: Alexandrov, Nikolai et al.
; TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
; FILE REFERENCE: 2750-1592PUS2
; CURRENT APPLICATION NUMBER: US/11/096,568A
; CURRENT FILING DATE: 2005-04-01
; NUMBER OF SEQ ID NOS: 34471
; SEQ ID NO 27942
; LENGTH: 983
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
; NAME/KEY: misc feature
; LOCATION: (1)..(983)
; OTHER INFORMATION: Ceres Seq. ID no. 2142330
US-11-096-568A-27942

Query Match 54.4%; Score 43; DB 7; Length 983;
Best Local Similarity 60.0%; Pred. No. 12;
Matches 9; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Qy 1 RHYGETKNQRRSSRS 15

Db 86 RKIGETSLNEVSSRS 100
| ||| :|: ||||

RESULT 30
US-11-096-568A-30324
; Sequence 30324, Application US/11096568A
; Publication No. US20060048240A1
; GENERAL INFORMATION:
; APPLICANT: Alexandrov, Nikolai et al.
; TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
; FILE REFERENCE: 2750-1592PUS2
; CURRENT APPLICATION NUMBER: US/11/096,568A
; CURRENT FILING DATE: 2005-04-01
; NUMBER OF SEQ ID NOS: 34471
; SEQ ID NO 30324
; LENGTH: 1039
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
; NAME/KEY: misc feature
; LOCATION: (1)..(1039)
; OTHER INFORMATION: Ceres Seq. ID no. 4953855
US-11-096-568A-30324

Query Match 54.4%; Score 43; DB 7; Length 1039;
Best Local Similarity 60.0%; Pred. No. 13;
Matches 9; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Qy 1 RHYGETKNQRRSSRS 15
| ||| :|: ||||
Db 177 RQIGETALNEVSSRS 191

RESULT 31
US-11-096-568A-30323
; Sequence 30323, Application US/11096568A
; Publication No. US20060048240A1
; GENERAL INFORMATION:
; APPLICANT: Alexandrov, Nikolai et al.
; TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
; FILE REFERENCE: 2750-1592PUS2
; CURRENT APPLICATION NUMBER: US/11/096,568A
; CURRENT FILING DATE: 2005-04-01
; NUMBER OF SEQ ID NOS: 34471
; SEQ ID NO 30323
; LENGTH: 1055
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
; NAME/KEY: misc feature
; LOCATION: (1)..(1055)
; OTHER INFORMATION: Ceres Seq. ID no. 4953854
US-11-096-568A-30323

Query Match 54.4%; Score 43; DB 7; Length 1055;
Best Local Similarity 60.0%; Pred. No. 13;
Matches 9; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Qy 1 RHYGETKNQRRSSRS 15
| ||| :|: ||||
Db 193 RQIGETALNEVSSRS 207

RESULT 32
US-11-096-568A-30322
; Sequence 30322, Application US/11096568A
; Publication No. US20060048240A1
; GENERAL INFORMATION:
; APPLICANT: Alexandrov, Nikolai et al.
; TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides

```
; TITLE OF INVENTION: Therby
; FILE REFERENCE: 2750-1592PUS2
; CURRENT APPLICATION NUMBER: US/11/096,568A
; CURRENT FILING DATE: 2005-04-01
; NUMBER OF SEQ ID NOS: 34471
; SEQ ID NO 30322
; LENGTH: 1063
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(1063)
; OTHER INFORMATION: Ceres Seq. ID no. 4953853
US-11-096-568A-30322
```

```
Query Match 54.4%; Score 43; DB 7; Length 1063;
Best Local Similarity 60.0%; Pred. No. 13;
Matches 9; Conservative 2; Mismatches 4; Indels 0; Gaps 0;
```

```
Qy 1 RHYGETKNQSRSS 15
| | | | | : | | | |
Db 201 RQIGETALNEVSSRS 215
```

```
RESULT 33
US-11-096-568A-27941
; Sequence 27941, Application US/11096568A
; Publication No. US20060048240A1
; GENERAL INFORMATION:
; APPLICANT: Alexandrov, Nickolai et al.
; TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
; FILE REFERENCE: 2750-1592PUS2
; CURRENT APPLICATION NUMBER: US/11/096,568A
; CURRENT FILING DATE: 2005-04-01
; NUMBER OF SEQ ID NOS: 34471
; SEQ ID NO 27941
; LENGTH: 1087
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(1087)
; OTHER INFORMATION: Ceres Seq. ID no. 2142329
US-11-096-568A-27941
```

```
Query Match 54.4%; Score 43; DB 7; Length 1087;
Best Local Similarity 60.0%; Pred. No. 13;
Matches 9; Conservative 2; Mismatches 4; Indels 0; Gaps 0;
```

```
Qy 1 RHYGETKNQSRSS 15
| | | | | : | | | |
Db 190 RKIGETSLNEVSSRS 204
```

```
RESULT 34
US-11-096-568A-34153
; Sequence 34153, Application US/11096568A
; Publication No. US20060048240A1
; GENERAL INFORMATION:
; APPLICANT: Alexandrov, Nickolai et al.
; TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
; FILE REFERENCE: 2750-1592PUS2
; CURRENT APPLICATION NUMBER: US/11/096,568A
; CURRENT FILING DATE: 2005-04-01
; NUMBER OF SEQ ID NOS: 34471
; SEQ ID NO 34153
; LENGTH: 970
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
; FEATURE:
; NAME/KEY: misc_feature
```

```
; LOCATION: (1)..(970)
; OTHER INFORMATION: Ceres Seq. ID no. 13605257
US-11-096-568A-34153
```

```
Query Match 51.9%; Score 41; DB 7; Length 970;
Best Local Similarity 60.0%; Pred. No. 27;
Matches 9; Conservative 1; Mismatches 5; Indels 0; Gaps 0;
```

```
Qy 1 RHYGETKNQSRSS 15
| | | | | : | | | |
Db 151 RATGSTNNNQSRSS 165
```

```
RESULT 35
US-11-096-568A-34152
; Sequence 34152, Application US/11096568A
; Publication No. US20060048240A1
; GENERAL INFORMATION:
; APPLICANT: Alexandrov, Nickolai et al.
; TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
; FILE REFERENCE: 2750-1592PUS2
; CURRENT APPLICATION NUMBER: US/11/096,568A
; CURRENT FILING DATE: 2005-04-01
; NUMBER OF SEQ ID NOS: 34471
; SEQ ID NO 34152
; LENGTH: 1035
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(1035)
; OTHER INFORMATION: Ceres Seq. ID no. 13605256
US-11-096-568A-34152
```

```
Query Match 51.9%; Score 41; DB 7; Length 1035;
Best Local Similarity 60.0%; Pred. No. 29;
Matches 9; Conservative 1; Mismatches 5; Indels 0; Gaps 0;
```

```
Qy 1 RHYGETKNQSRSS 15
| | | | | : | | | |
Db 216 RATGSTNNNQSRSS 230
```

```
RESULT 36
US-11-096-568A-34151
; Sequence 34151, Application US/11096568A
; Publication No. US20060048240A1
; GENERAL INFORMATION:
; APPLICANT: Alexandrov, Nickolai et al.
; TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
; FILE REFERENCE: 2750-1592PUS2
; CURRENT APPLICATION NUMBER: US/11/096,568A
; CURRENT FILING DATE: 2005-04-01
; NUMBER OF SEQ ID NOS: 34471
; SEQ ID NO 34151
; LENGTH: 1042
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(1042)
; OTHER INFORMATION: Ceres Seq. ID no. 13605255
US-11-096-568A-34151
```

```
Query Match 51.9%; Score 41; DB 7; Length 1042;
Best Local Similarity 60.0%; Pred. No. 29;
Matches 9; Conservative 1; Mismatches 5; Indels 0; Gaps 0;
```

```
Qy 1 RHYGETKNQSRSS 15
| | | | | : | | | |
Db 223 RATGSTNNNQSRSS 237
```

```
RESULT 37
US-11-082-389-84
; Sequence 84, Application US/11082389
; Publication No. US20050244935A1
; GENERAL INFORMATION:
; APPLICANT: Pompejus, Markus
; APPLICANT: Krogger, Burkhard
; APPLICANT: Schroder, Hartwig
; APPLICANT: Zelder, Oskar
; APPLICANT: Haberhauer, Gregor
; TITLE OF INVENTION: CORYNEBACTERIUM GLUTAMICUM GENES ENCODING PROTEINS
; TITLE OF INVENTION: INVOLVED IN MEMBRANE SYNTHESIS AND MEMBRANE
; TITLE OF INVENTION: TRANSPORT
; FILE REFERENCE: BGI-131CPCN
; CURRENT APPLICATION NUMBER: US/11/082,389
; PRIOR FILING DATE: 2005-03-16
; PRIOR APPLICATION NUMBER: US 09/603024
; PRIOR FILING DATE: 2000-06-23
; PRIOR APPLICATION NUMBER: US 60/141031
; PRIOR FILING DATE: 1998-06-25
; PRIOR APPLICATION NUMBER: US 60/143262
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: US 60/151281
; PRIOR FILING DATE: 1999-08-27
; PRIOR APPLICATION NUMBER: DE 19930487.4
; PRIOR FILING DATE: 1998-07-01
; PRIOR APPLICATION NUMBER: DE 19930489.0
; PRIOR FILING DATE: 1999-07-01
; PRIOR APPLICATION NUMBER: DE 19931549.3
; PRIOR FILING DATE: 1999-07-08
; PRIOR APPLICATION NUMBER: DE 19931550.7
; PRIOR FILING DATE: 1999-07-08
; PRIOR APPLICATION NUMBER: DE 19932134.5
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: DE 19941379.7
; PRIOR FILING DATE: 1999-08-31
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 446
; SEQ ID NO 84
; LENGTH: 302
; TYPE: PRT
; ORGANISM: Corynebacterium glutamicum
US-11-082-389-84

Query Match          50.6%; Score 40; DB 7; Length 302;
Best Local Similarity 53.3%; Pred. No. 12;
Matches 8; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY      1 RHYGETKNQRSRS 15
      |||||
DB      287 RHYGETVSGSEKAS 301

RESULT 38
US-11-087-099-3831
; Sequence 3831, Application US/11087099
; Publication No. US20060041961A1
; GENERAL INFORMATION:
; APPLICANT: Abad, Mark S. et al.
; TITLE OF INVENTION: Genes and Uses for Plant Improvement
; FILE REFERENCE: 38-21(53450)B EP
; CURRENT APPLICATION NUMBER: US/11/087,099
; CURRENT FILING DATE: 2005-03-22
; NUMBER OF SEQ ID NOS: 12464
; SEQ ID NO 3831
; LENGTH: 1142
; TYPE: PRT
; ORGANISM: Saccharomyces cerevisiae
US-11-087-099-3831

Query Match          50.6%; Score 40; DB 7; Length 1142;
```

```
Best Local Similarity 61.5%; Pred. No. 49;
Matches 8; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY      3 YGETKNQRSRS 15
      :|||:|||||
DB      485 FSTTKNKRSSRS 497

RESULT 39
US-11-079-463-10327
; Sequence 10327, Application US/11079463
; Publication No. US20060073161A1
; GENERAL INFORMATION:
; APPLICANT: Gary L. Breton
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO BACTEROIDES FR
; FILE REFERENCE: PATH00-03DIV2
; CURRENT APPLICATION NUMBER: US/11/079,463
; CURRENT FILING DATE: 2005-03-14
; PRIOR APPLICATION NUMBER: US 60/128,705
; PRIOR FILING DATE: 1999-04-09
; PRIOR APPLICATION NUMBER: US 09/540,209
; PRIOR FILING DATE: 2000-04-04
; NUMBER OF SEQ ID NOS: 10444
; SEQ ID NO 10327
; LENGTH: 453
; TYPE: PRT
; ORGANISM: B. fragilis
US-11-079-463-10327

Query Match          48.1%; Score 38; DB 7; Length 453;
Best Local Similarity 60.0%; Pred. No. 43;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY      2 HYGETKNQR 11
      ||:|||||
DB      15 HYSKTSMNKR 24

RESULT 40
US-11-188-298-19543
; Sequence 19543, Application US/11188298
; Publication No. US20060075522A1
; GENERAL INFORMATION:
; APPLICANT: Abad, Mark S. et al.
; TITLE OF INVENTION: GENES AND USES FOR PLANT IMPROVEMENT
; FILE REFERENCE: 38-21(53452)B
; CURRENT APPLICATION NUMBER: US/11/188,298
; CURRENT FILING DATE: 2005-07-22
; PRIOR APPLICATION NUMBER: 60/592,978
; PRIOR FILING DATE: 2004-07-31
; NUMBER OF SEQ ID NOS: 22569
; SEQ ID NO 19543
; LENGTH: 506
; TYPE: PRT
; ORGANISM: ASPERGILLUS NIDULANS FGSC A4
US-11-188-298-19543

Query Match          48.1%; Score 38; DB 7; Length 506;
Best Local Similarity 57.1%; Pred. No. 48;
Matches 8; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY      2 HYGETKNQRSRS 15
      |:|||||
DB      466 HAEKQLNARSRS 479

RESULT 41
US-10-506-454-292
; Sequence 292, Application US/10506454
; Publication No. US20060068386A1
; GENERAL INFORMATION:
; APPLICANT: Slesarev, Alexi I
```

; APPLICANT: Mezheva, Katja V
; APPLICANT: Poluehin, Nikolai N
; APPLICANT: Shcherbinina, Olga V
; APPLICANT: Shakhova, Vera V
; APPLICANT: Malykh, Andrei G
; APPLICANT: Kozavkin, Sergei A
; TITLE OF INVENTION: The Complete Genome and Protein Sequences of the Hyperthermophile
; TITLE OF INVENTION: Methanopyrus Kandleri AV19 and Monophyly of Archaeal Methanogens
; TITLE OF INVENTION: and Methods of Use Thereof
; FILE REFERENCE: FID001
; CURRENT APPLICATION NUMBER: US/10/506,454
; CURRENT FILING DATE: 2004-08-31
; PRIOR APPLICATION NUMBER: PCT/US03/06664
; PRIOR FILING DATE: 2003-03-04
; PRIOR APPLICATION NUMBER: 60/361,742
; PRIOR FILING DATE: 2002-03-04
; NUMBER OF SEQ ID NOS: 1722
; SOFTWARE: Patentin version 3.2
; SEQ ID NO 292
; LENGTH: 290
; TYPE: PRT
; ORGANISM: Methanopyrus kandleri
US-10-506-454-292

Query Match 46.8%; Score 37; DB 6; Length 290;
Best Local Similarity 85.7%; Pred. No. 41;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RHYGETK 7
Db 50 RHYGETE 56
|||||:

RESULT 42
US-11-098-686-11287
; Sequence 11287, Application US/11098686
; Publication No. US20060024696A1
; GENERAL INFORMATION:
; APPLICANT: Kapur, Vivek and Gebhart, Connie J.
; TITLE OF INVENTION: NUCLEIC ACID AND POLYPEPTIDE SEQUENCES
; TITLE OF INVENTION: FROM LAWSONIA INTRACELLULARIS AND METHODS OF USING
; FILE REFERENCE: 09531-128001
; CURRENT APPLICATION NUMBER: US/11/098,686
; CURRENT FILING DATE: 2005-04-04
; PRIOR APPLICATION NUMBER: PCT/US03/31318
; PRIOR FILING DATE: 2003-10-01
; PRIOR APPLICATION NUMBER: US 60/416,395
; PRIOR FILING DATE: 2002-10-04
; NUMBER OF SEQ ID NOS: 11433
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11287
; LENGTH: 334
; TYPE: PRT
; ORGANISM: Lawsonia intracellularis
US-11-098-686-11287

Query Match 46.8%; Score 37; DB 7; Length 334;
Best Local Similarity 50.0%; Pred. No. 47;
Matches 6; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 3 YGETKMNQRSSR 14
:|||||:
Db 33 FGQTKMNSGTR 44

RESULT 43
US-11-098-686-10227
; Sequence 10227, Application US/11098686
; Publication No. US20060024696A1
; GENERAL INFORMATION:
; APPLICANT: Kapur, Vivek and Gebhart, Connie J.
; TITLE OF INVENTION: NUCLEIC ACID AND POLYPEPTIDE SEQUENCES
; TITLE OF INVENTION: FROM LAWSONIA INTRACELLULARIS AND METHODS OF USING

; FILE REFERENCE: 09531-128001
; CURRENT APPLICATION NUMBER: US/11/098,686
; CURRENT FILING DATE: 2005-04-04
; PRIOR APPLICATION NUMBER: PCT/US03/31318
; PRIOR FILING DATE: 2003-10-01
; PRIOR APPLICATION NUMBER: US 60/416,395
; PRIOR FILING DATE: 2002-10-04
; NUMBER OF SEQ ID NOS: 11433
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10227
; LENGTH: 353
; TYPE: PRT
; ORGANISM: Lawsonia intracellularis
US-11-098-686-10227

Query Match 46.8%; Score 37; DB 7; Length 353;
Best Local Similarity 53.8%; Pred. No. 50;
Matches 7; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 2 HYGETKMNQRSSR 14
|||||:
Db 231 HYGETLSQLPSR 243

RESULT 44
US-11-087-099-422
; Sequence 422, Application US/11087099
; Publication No. US20060041961A1
; GENERAL INFORMATION:
; APPLICANT: Abad, Mark S. et al.
; TITLE OF INVENTION: Genes and Uses for Plant Improvement
; FILE REFERENCE: 38-21(53450)B EP
; CURRENT APPLICATION NUMBER: US/11/087,099
; CURRENT FILING DATE: 2005-03-22
; NUMBER OF SEQ ID NOS: 12464
; SEQ ID NO 422
; LENGTH: 575
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
US-11-087-099-422

Query Match 46.8%; Score 37; DB 7; Length 575;
Best Local Similarity 57.1%; Pred. No. 83;
Matches 8; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 2 HYGETKMNQRSSR 15
|||||:
Db 415 HMLETRQSRSSSS 428

RESULT 45
US-11-096-568A-29274
; Sequence 29274, Application US/11096568A
; Publication No. US20060048240A1
; GENERAL INFORMATION:
; APPLICANT: Alexandrov, Nikolai et al.
; TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
; TITLE OF INVENTION: Thereby
; FILE REFERENCE: 2750-1592PUS2
; CURRENT APPLICATION NUMBER: US/11/096,568A
; CURRENT FILING DATE: 2005-04-01
; NUMBER OF SEQ ID NOS: 34471
; SEQ ID NO 29274
; LENGTH: 1145
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana

; FEATURE:
; NAME/KEY: misc.feature
; LOCATION: (1)..(1145)
; OTHER INFORMATION: Ceres Seq. ID no. 4805154
US-11-096-568A-29274

Query Match 46.8%; Score 37; DB 7; Length 1145;

Best Local Similarity 53.3%; Pred. No. 1.7e+02; Mismatches 5; Indels 0; Gaps 0;
Matches 8; Conservative 2;
QY 1 RHYGETKNQRRSSRS 15
DB 632 RAVGKTTANEHSSRS 646

RESULT 46
US-11-096-568A-29273
; Sequence 29273, Application US/11096568A
; Publication No. US20060048240A1
; GENERAL INFORMATION:
; APPLICANT: Alexandrov, Nikolai et al.
; TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
; FILE OF INVENTION: Therby
; CURRENT APPLICATION NUMBER: US/11/096,568A
; CURRENT FILING DATE: 2005-04-01
; NUMBER OF SEQ ID NOS: 34471
; SEQ ID NO 29273
; LENGTH: 1160
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)-(1160)
; OTHER INFORMATION: Ceres Seq. ID no. 4805153
US-11-096-568A-29273

Query Match 46.8%; Score 37; DB 7; Length 1160;
Best Local Similarity 53.3%; Pred. No. 1.7e+02; Mismatches 5; Indels 0; Gaps 0;
Matches 8; Conservative 2;
QY 1 RHYGETKNQRRSSRS 15
DB 647 RAVGKTTANEHSSRS 661

RESULT 47
US-11-096-568A-29272
; Sequence 29272, Application US/11096568A
; Publication No. US20060048240A1
; GENERAL INFORMATION:
; APPLICANT: Alexandrov, Nikolai et al.
; TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
; FILE REFERENCE: 2750-1592PUS2
; CURRENT APPLICATION NUMBER: US/11/096,568A
; CURRENT FILING DATE: 2005-04-01
; NUMBER OF SEQ ID NOS: 34471
; SEQ ID NO 29272
; LENGTH: 1195
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)-(1195)
; OTHER INFORMATION: Ceres Seq. ID no. 4805152
US-11-096-568A-29272

Query Match 46.8%; Score 37; DB 7; Length 1195;
Best Local Similarity 53.3%; Pred. No. 1.8e+02; Mismatches 5; Indels 0; Gaps 0;
Matches 8; Conservative 2;
QY 1 RHYGETKNQRRSSRS 15
DB 682 RAVGKTTANEHSSRS 696

RESULT 48
US-11-045-004-1154
; Sequence 1154, Application US/11045004

Publication No. US20060078901A1
; GENERAL INFORMATION:
; APPLICANT: BUCHRIESER, CARMEN
; APPLICANT: FRANGEUL, LIONEL
; APPLICANT: COUVE, ELISABETH
; APPLICANT: RUSNIOK, CHRISTOPHE
; APPLICANT: FSIHI, HAFIDA
; APPLICANT: DEHOUX, PIERRE
; APPLICANT: DUSURGET, OLIVIER
; APPLICANT: CHETOUANI, FARID
; APPLICANT: NEDJARI, HAFED
; APPLICANT: GLASER, PHILIPPE
; APPLICANT: KUNST, FRANCK
; APPLICANT: COSSAET, PASCALE
; APPLICANT: DANIELS, JUSTIN
; APPLICANT: GOEBEL, WERNER
; APPLICANT: KREFT, JURGEN
; APPLICANT: KUHN, MICHAEL
; APPLICANT: NG, EVA
; APPLICANT: VAZQUEZ-BOLAND, ANTONIO
; APPLICANT: DOMINGUEZ-BERNAL, GUSTAVO
; APPLICANT: GARRIDO-GARCIA, PATRICIA
; APPLICANT: TIERREZ-MARTINEZ, ALBERTO
; APPLICANT: AMEND, ALEXANDRA
; APPLICANT: CHAGRABORTY, TRINAD
; APPLICANT: DOMANN, EUGEN
; APPLICANT: HAIN, THORSTEN
; APPLICANT: BERCHE, PATRICK
; APPLICANT: CHARBIT, ALAIN
; APPLICANT: DURANT, LIONEL
; APPLICANT: PEREZ-DIAZ, JOSE-CLAUDIO
; APPLICANT: BAQUERO, FERNANDO
; APPLICANT: GARCIA DEL PORTILLO, FRANCISCO
; APPLICANT: GOMEZ-LOPEZ, NURIA
; APPLICANT: MADUENIO, ENCARN
; APPLICANT: PABLOS, BETRIZ DE
; APPLICANT: WEHLAND, JURGEN
; APPLICANT: KARST, UWE
; APPLICANT: ENTIAN, KARL-DIETER
; APPLICANT: HAUF, JORG
; APPLICANT: ROSE, MATTHIAS
; APPLICANT: VOSS, HAMUT
; TITLE OF INVENTION: LISTERIA MONOCYTOGENES GENOME, POLYPEPTIDES AND USES
; FILE REFERENCE: 05394.0018-02
; CURRENT APPLICATION NUMBER: US/11/045,004
; CURRENT FILING DATE: 2005-01-28
; PRIOR APPLICATION NUMBER: 10/637,657
; PRIOR FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: 10/257,023
; PRIOR FILING DATE: 2002-10-08
; PRIOR APPLICATION NUMBER: PCT/FR01/01118
; PRIOR FILING DATE: 2001-04-11
; PRIOR APPLICATION NUMBER: FR 00/04,629
; PRIOR FILING DATE: 2000-04-11
; NUMBER OF SEQ ID NOS: 2854
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1154
; LENGTH: 204
; TYPE: PRT
; ORGANISM: Listeria monocytogenes
US-11-045-004-1154

Query Match 45.6%; Score 36; DB 7; Length 204;
Best Local Similarity 54.5%; Pred. No. 43; Mismatches 3; Indels 0; Gaps 0;
Matches 6; Conservative 3;
QY 2 HYGETKNQRS 12
DB 65 YYGKEKNQES 75

RESULT 49
US-11-188-298-20356

; Sequence 20356, Application US/11188298
; Publication No. US20060075522A1
; GENERAL INFORMATION:
; APPLICANT: Abad, Mark S. et al.
; TITLE OF INVENTION: GENES AND USES FOR PLANT IMPROVEMENT
; FILE REFERENCE: 38-21(53452)B
; CURRENT APPLICATION NUMBER: US/11/188,298
; CURRENT FILING DATE: 2005-07-22
; PRIOR APPLICATION NUMBER: 60/592,978
; PRIOR FILING DATE: 2004-07-31
; NUMBER OF SEQ ID NOS: 22569
; SEQ ID NO 20356
; LENGTH: 313
; TYPE: PRT
; ORGANISM: Cicer arietinum
US-11-188-298-20356

Query Match 45.6%; Score 36; DB 7; Length 313;
Best Local Similarity 72.7%; Pred. No. 67;
Matches 8; Conservative 1; Mismatches 0; Indels 2; Gaps 1;

QY 1 RHYGETKMNQR 11
Db 64 RHY--SKMNQR 72

RESULT 50
US-11-152-569-12
; Sequence 12, Application US/11152569
; Publication No. US20060005278A1
; GENERAL INFORMATION:
; APPLICANT: Ecker, Joseph R.
; APPLICANT: Nehring, Ramlaah
; APPLICANT: McGrath, Robert B.
; TITLE OF INVENTION: ETHYLENE INSENSITIVE PLANTS
; FILE REFERENCE: 532792001210
; CURRENT APPLICATION NUMBER: US/11/152,569
; CURRENT FILING DATE: 2005-06-13
; PRIOR APPLICATION NUMBER: 10/144,156
; PRIOR FILING DATE: 2002-10-05
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12
; LENGTH: 317
; TYPE: PRT
; ORGANISM: Schizosaccharomyces pombe
US-11-152-569-12

Query Match 45.6%; Score 36; DB 7; Length 317;
Best Local Similarity 62.5%; Pred. No. 68;
Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 RHYGETKM 8
Db 179 QHYGDTKL 186

Search completed: April 21, 2006, 13:57:21
Job time : 34 secs

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